

STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 189439

TO: Andrew D Kosar
Location: 3c04 / 3c18
Art Unit: 1654
Wednesday, May 10, 2006

Case Serial Number: 10/800179

From: Noble Jarrell
Location: Biotech-Chem Library
Rem 1B71
Phone: 272-2556

Noble.jarrell@uspto.gov

Search Notes

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189439

STIC-Biotech/ChemLib

From: ANDREW KOSAR [andrew.kosar@uspto.gov]
Sent: Tuesday, May 09, 2006 5:16 PM
To: STIC-Biotech/ChemLib
Subject: Database Search Request, Serial Number: 10/800,179

Requester:
ANDREW KOSAR (P/1654)
Art Unit:
GROUP ART UNIT 1654
Employee Number:
80341
Office Location:
REM 03C04
Phone Number:
(571)272-0913
Mailbox Number:
REM 3c18

Case serial number:
10/800,179
Class / Subclass(es):

Earliest Priority Filing Date:

Format preferred for results:
Paper

Search Topic Information:
Please search SEQ ID NO:19 in 10/800,179.


Special Instructions and Other Comments:

Searcher: Noble
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: 5/12/06
Searcher Prep Time: 5
Online Time: 5

Type of Search
NA# _____ AA#: 1
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: Compugen
WWW/Internet: _____
Other (Specify): _____

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 **PALM INTRANET**

Day : Wednesday

Date: 5/10/2006

Time: 16:58:59

Inventor Information for 10/800179

Inventor Name	City	State/Country
KUMAR, MANOJ	FREMONT	CALIFORNIA
CUEVAS, WILLIAM A.	SAN FRANCISCO	CALIFORNIA

Appln Info	Contents	Petition Info	Atty/Agent Info	Continuity Data	Foreign Data	Inventor
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Search Another: Application# Search or Patent# Search

PCT / / Search or PG PUBS # Search

Attorney Docket # Search

Bar Code # Search

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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Result No.	Score	Query Match	Length	DB	ID	Description
1	1353	32.4	784	2	A26601	elastin precursor
2	1218	29.2	860	1	EAMS	elastin precursor
3	1185	28.4	864	1	EART	elastin precursor
4	1151	27.6	747	1	EABO	elastin precursor
5	1146.5	27.5	770	2	S59623	tropoelastin - sh
6	1137	27.2	713	1	UMMS	period clock prot
7	1096	26.3	1901	2	F70806	hypothetical glyce
8	1089.5	26.0	1079	2	B70807	hypothetical glyce
9	1084	25.0	1489	2	D70807	hypothetical glyce
10	1055.5	25.3	792	1	EAHU	elastin precursor
11	1041	24.9	718	2	A36068	major ampullate f
12	1034	24.8	1660	2	A70869	hypothetical glyce
13	1010.5	24.2	1329	2	E70917	hypothetical glyce
14	1006	24.1	1381	2	E70806	hypothetical glyce
15	984	23.6	1306	2	A70934	hypothetical glyce
16	965	23.1	1538	2	H70846	hypothetical glyce
17	961	23.0	408	2	S57483	glycin-rich prote
18	955	22.9	882	2	B70812	hypothetical glyce
19	942.5	22.6	749	2	A70812	hypothetical glyce
20	940.5	22.5	853	2	A70896	hypothetical glyce
21	888	21.3	914	2	H70987	hypothetical glyce
22	886	21.1	718	2	F70963	hypothetical glyce
23	879	20.7	957	2	D70835	hypothetical glyce
24	862	20.7	13288	2	T03099	hypothetical glyce
25	846	20.3	767	2	E70895	nucin, submaxilla
26	845.5	20.3	837	2	E70835	hypothetical glyce
27	842	20.2	465	1	S01820	hypothetical glyce
28	826.5	19.8	641	1	Q0E31	glycine-rich cell
29	825	19.8	2639	2	T31338	nuclear antigen E
						fibroin - Chinese

30	822.5	19.7	384	1	A26099	glycine-rich cell
31	817	19.6	801	2	F30824	hypothetical glycp
32	805	19.3	338	1	KNNU	glycine-rich cell
33	779.5	18.7	783	2	E70824	hypothetical glycp
34	766.5	18.4	1466	1	CGHU74	collagen alpha 1(I)
35	761.5	18.2	1585	2	T31611	hypothetical prote
36	757.5	18.1	741	2	G70917	hypothetical glycp
37	753.5	18.2	1049	1	CG8078	collagen alpha 1(I)
38	751	18.0	627	2	A44112	spiroidin 2, dragli
39	750.5	18.0	714	2	A70807	hypothetical glycp
40	742	17.8	336	2	T49109	glycine-rich prote
41	740.5	17.7	1958	2	B4505	hypothetical prote
42	739	17.7	1669	1	CGHU48	collagen alpha 1(I)
43	738.5	17.7	1464	2	S5886	collagen alpha 1(I)
44	727.5	17.4	667	2	A70893	hypothetical glycp
45	725.5	17.4	1464	1	CGHU15	collagen alpha 1(I)

ALIGNMENTS

```

RESULT 1
A26601
elastin precursor - chicken (fragment)
N.Alternate names: tropoelastin
C.Species: Gallus gallus (chicken)
C.Date: 05-oct-1988 #sequence revision 26-Jul-1996 #text_change 09-Jul-2004
C.Accession: A26601; A30795; A27264
R.Bressan, G.M.; Argos, P.; Stanley, K.K.
Biochemistry 26, 1497-1503, 1987
A.Title: Repeating structure of chick tropoelastin revealed by complementary DNA cloning
A.Reference number: A26601; MUID:87242320; PMID:3593675
A.Accession: A26601
A.Molecule type: mRNA
A.Residues: 1-212,237-524,535-784 <BR2>
A.Cross-references: UNIPROT:P07916; UNIPARC:UPI0000129E6D; GB:M15889; NID:G212803; PIDN:A:
R.Baule, V.J.; Foster, J.A.
Biochem. Biophys. Res. Commun. 154, 1054-1060, 1988
A.Title: Multiple chick tropoelastin mRNAs.
A.Reference number: A30795; MUID:88309083; PMID:2841924
A.Accession: A30795
A.Molecule type: mRNA
A.Residues: 85-784 <BAU>
A.Cross-references: UNIPARC:UPI0000171B34; GB:M21880; NID:G212741; PIDN:AAA49082.1; PID:
R.Tokimitsu, I.; Tajima, S.; Nishikawa, T.; Tajima, M.; Fukasawa, T.
Arch. Biochem. Biophys. 256, 455-461, 1987
A.Title: Sequence analysis of elastin cDNA from chick aorta and tissue-specific transcrip
A.Reference number: A27264; MUID:87297534; PMID:3502711
A.Accession: A27264
A.Molecule type: mRNA
A.Residues: 491-569, 'G', 571-604, 'A', 606-643, 'A', 645-687, 'R', 689-700, 'R', 702-784 <TOK>
A.Cross-references: UNIPARC:UPI0000156DBE; GB:M18633; NID:G211742; PIDN:AAA48761.1; PID:
C.Superfamily: elastin
C.Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F.1-34/Domains: signal sequence (fragment) #status predicted <SIG>
F.21-212,237-524,535-784/Product: elastin #status predicted <MAT>
F.1773-779/Disulfide bonds: #status predicted

Query Match          32.4%; Score 1353; DB 2; Length 784;
Best Local Similarity 48.0%; Pred. No. 8.7e-75;
Matches 409; Conservative 37; Mismatches 188; Indels 218; Gaps 68;

Oy      16 VPGV-----GVPGVPKGKVGPGVGPVGPGVGPVGPGAGAGSGAGAGSGA 62
       :|||               |||   |||   :|||   |||   |||
Db      9 LRGVLLLSILPASQGGVPG--AIRGCVP-----CGGFPPGAVG----GLGA 52

Oy      63 GAGSGAGAGSGVGVPGV--GVPGV---VPGKGVPGVPGV-----PGVPGVPGA 110
       :|||   |||   |||   |||   :|||   :|||   :|||
Db     53 GLGAGLGGAGKRPLKPGVSGLGLGPLQLPGAGVGGLAGLGAFPGAAPGAASAAALKA 112

Oy     111 GAGSGAGAG-----SGAGAGSGAGAGSGVGPVGVPVG-----VPGKGVPGVPGV 158
       :|||   |||   |||   |||   :|||   :|||   :|||
Db    113 AAAGAAGLGGVGGIGLGGVGGVGPVGGLGVPVGVPVGVAAGKPKPYCPGAGIGAPFGG 172

```


A/Accession: B26728
 A/Molecule type: mRNA
 A/Residues: 1,'RS',4-11,'E',13-225,240-636,'V',638-747 <RA2>
 A/Cross-references: UNIPARC:UPI000002ABD3; GB:K03505; NID:g163025; PIDN:AAA30505.1; PID:
 A/Accession: C26728
 A/Molecule type: mRNA
 A/Residues: 1,'RS',4-11,'E',13-225,260-636,'V',638-747 <RA3>
 A/Cross-references: UNIPARC:UPI000002ABD4; GB:K03506; NID:g163027; PIDN:AAA30506.1; PID:
 R.Cicilia, G.; May, M.; Ornstein-Goldstein, N.; Indik, Z.; Morrow, S.; Yeh, H.S.; Rosenbl
 Biochemistry 24, 3075-3080, 1985
 A/Title: Structure of the 3' portion of the bovine elastin gene.
 A/Reference number: A22343; MUID:85280426; PMID:2992576
 A/Accession: A22343
 A/Molecule type: DNA
 A/Residues: 613-747 <C1C>
 A/Cross-references: UNIPARC:UPI0000173C4F; GB:M20415
 R.Rosenbloom, J.
 Lab. Invest. 51, 605-623, 1984
 A/Title: Biology of disease: Elastin: Relation of protein and gene structure to disease.
 A/Reference number: 145885; MUID:85059254; PMID:6150137
 A/Accession: 145886
 A/Status: preliminary; translated from GB/EMBL/DBET
 A/Molecule type: DNA
 A/Residues: 678-683,685-747 <ROS>
 A/Cross-references: UNIPARC:UPI000008856A; GB:M31898; NID:g163015; PIDN:AAA96417.1; PID:
 R.Brown, P.L.; Mecham, L.; Tiedale, C.; Mecham, R.P.
 Biochem. Biophys. Res. Commun. 186, 549-555, 1992
 A/Title: The cysteine residues in the carboxy terminal domain of tropoelastin form an in
 A/Reference number: A58621; MUID:92337651; PMID:1632791
 A/Contents: annotation, disulfide bonds
 C/Comment: The term tropoelastin refers to a soluble precursor form of the extracellular
 line oxidase activity.
 C/Genetics: 634/3, 653/3, 676/3, 689/3, 707/3, 716/3, 733/3
 A/Intons: 634/3, 653/3, 676/3, 689/3, 707/3, 716/3, 733/3
 A/Note: the list of introns is incomplete
 C/Superfamily: elastin
 C/Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
 F:1-747/Product: elastin precursor, splice form a #status predicted <EPA>
 F:1-225,260-747/Product: elastin precursor, splice form c #status predicted <EPC>
 F:1-225,280-747/Product: elastin precursor, splice form b #status predicted <EPB>
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:1-747/Product: elastin #status predicted <MAT>
 F:105,109,252,271,275,324,327,400,404,407,445,448,489,493,544,548,552,606,609,645,649,68
 F:737-742/Disulfide bonds: #status experimental

Query Match 27.6%; Score 1151; DB 1; Length 747;
 Best Local Similarity 41.4%; Pred. No. 1.1e-62;
 Matches 350; Conservative 46; Mismatches 249; Indels 200; Gaps 45;

QY 5 GSGAGSGGVVP-GVGVPGVPGKGVPGVPGG-----VGPGV-----PGA 50
 DB 27 GGVPGVAVPG-GVPGGVFPFGAGIGLGGVGLGPGVPAKKGCGVLGPGLAGAGSLPGA 85
 QY 51 GAGSGAGAGSG-AGAGSGAGAGSGGVPGVPGVPGKGVPGVPGVPGVPGVPGV 109
 DB 86 PFGGFFGAGAGGAAGAAAKAAKAAAGAGVGIG-----GVGGIGVSTG-----AVVPQ 136
 QY 110 AAGAGAGAGSGAGAGSGAGAGSGGVPGVPGVPGKGVPGV-----PGVPGVPGV 166
 DB 137 LGAGVAGVAPGK-----VPGVGLPGV-YPGVGLPGAGARFPGI--GVLPGV 180
 QY 167 GGGAGAGSGAGAGSGAGAGSGGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 223
 DB 181 PTGAGVAPKPAQVAGAF-----GIPGVPGGGQGPGLPTPIAPKPLPAGYGL 230
 QY 224 -----PGVPGAGAGSGAGAGSGAGSG-----AGAGSGGVPGVPGVPGVPGV 267
 DB 231 PYKTGKLPYFGFGGAGVAGSAGKAGPYTGTVGVPQAAAAAKAAKXGAGAGVLPVGVG 290
 QY 268 GKGVPVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 327
 DB 291 GPGIPG-----APGAIPTGIGIVGAPDAAAAAAAAAAAAKAKFAGAGLPGVGVPGV 345

QY 328 GKGVPVPGV-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGGVPGVPGVPG 383
 DB 346 GGVPGVPGVPGVPGVPGVPGVPGVPGVPGV-----PGVPGVPGVPG 386
 QY 384 VGVPG-----KGVPGVP-----GVPGVPGVPGVPGAGSGAGAGS 420
 DB 387 VGVPGALSPAATAKAAKAKFGARCAVGIGIPTFGLPBGCFPGIGDAAAAPAA----- 442
 QY 421 GAGAGSGAGAGSGGVPGVPGVPGVPGKGVPGVPGVPGVPGVPGVPGVPGVPGV 477
 DB 443 -----AAKAKTIGAGTIGALGVPG--GABATIGL-PGVGVGVTGIPAAAAAKAAA 492
 QY 478 AGSGAGAGSGAGAGSGGVPGVPGVPGVPGKGVPGVPGVPGVPGVPGVPGVPGV 537
 DB 493 KAAFGGLGPGVAVPAGV-----VPGV-----GVAPGIGLPGGVIGAGVPA 542
 QY 538 AGSGAGAGSGAGAGSGGVPGVPGVPGVPGKGVPGVPGVPGVPGVPGVPGVPGV 593
 DB 543 AKAAPAAKAAKAPRAAAGLP-AGVPLGV-GAGVPLGVAGAGVPGVPGVPAVPG 600
 QY 594 SGAGSGAGAGSGAGAGSGGVPGVPGVPGVPGVPGKGVPGVPGVPGVPGVPGV 653
 DB 601 TLAAPAAKAPREGVAGLGGVDLG---GAGIPG-GVAGVGP----- 638
 QY 654 SGAGSGAGAGSGAGAGSGGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 712
 DB 639 --AAAAAARAAKAAKAPFGLG-GVGLGVGGLGAVPG---AVGLG---GVSPAAAAKAAK 688
 QY 713 GSGAGAGSGAGAGSGAGAGSGGVPGVPGVPGVPGKGVPGVPGVPGVPGVPGVPGV 772
 DB 689 PGAAAGLGVLAGAGQPPPIGGAG-----GLGVGKPKPPFGGALGALGFP---GACL 738
 QY 773 GSGAG 777
 DB 739 GASCAG 743

RESULT 5
 S59623
 tropoelastin - sheep
 C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C/Date: 23-Aug-1996 #sequence_rev15on 13-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S59623, A24758
 R/Nauch, J.C.; Sandberg, L.B.; Roos, P.J.; Jimenez, F.; Christiano, A.M.; Deak, S.B.; Boy
 Matrix Biol. 14, 635-641, 1994
 A/Title: Extensive alternate exon usage at the 5' end of the sheep tropoelastin gene.
 A/Reference number: S59623
 A/Status: preliminary; not compared with conceptual translation
 A/Accession: S59623
 A/Molecule type: mRNA
 A/Residues: 1-770 <MAN>
 A/Cross-references: UNIPROT:P11547; UNIPARC:UPI0000177409
 R/Toom, K.; Davidson, J.M.; Boyd, C.; May, M.; Luvallie, P.; Ornstein-Goldstein, N.; Smilt
 Arch. Biochem. Biophys. 241, 684-691, 1985
 A/Title: Analysis of the 3' region of the sheep elastin gene.
 A/Reference number: A24758; MUID:85305763; PMID:3839997
 A/Accession: A24758
 A/Molecule type: mRNA
 A/Residues: 655-669,671-716,732-770 <YOO>
 A/Cross-references: UNIPARC:UPI0000129E70
 C/Superfamily: elastin
 C/Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
 F:760-765/Disulfide bonds: #status predicted

Query Match 27.5%; Score 1146.5; DB 2; Length 770;
 Best Local Similarity 42.5%; Pred. No. 2.1e-62;
 Matches 368; Conservative 41; Mismatches 239; Indels 217; Gaps 52;

QY 5 GSGAGSGGVVP-GVGVPGVPGKGVPGVPGV-----GPGVPGVPGAGAG--GSGA--- 56
 DB 27 GGVLAGVAVPG-GVPGGVFPFGAGIGLGGVGLGPGVPAKKGCGVLGPGLAGAGSGSLPA 85
 QY 57 -----GAGSGAG-----AGSGAGAGSGGVPGVPGVPGVPGKGVPGVPGVPG 101

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2006, 10:36:23 ; Search time 232 Seconds
(without alignment)

2372.035 Million cell updates/sec

Title: US-10-800-179-19

Sequence: 1 GAGAGSGAGAGSGVGPVGVG.....GVGPVGPAGAGSGAGAGS 780

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database :

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2107.5	50.5	5263	1	FIBH_BOMMO
2	1916.5	45.9	897	2	O6O2S4_AGEAP
3	1531	36.7	760	2	O6PY84_KUKAI
4	1459.5	35.0	1002	2	O9BI08_ARGTR
5	1451.5	34.8	988	2	O17434_NBPCL
6	1397.5	33.5	1553	2	O6FPR0_CANGA
7	1365	32.7	1884	2	O9NHW2_9ARAC
8	1314	31.5	750	1	ELN_CHICK
9	1312.5	31.5	1713	2	O9VTR6_DROME
10	1302.5	31.2	912	2	O9BIR2_PLETR
11	1302.5	31.2	2249	2	O9NHM4_NBPCL
12	1297.5	31.1	1953	2	O9BIR7_9ARAC
13	1274	30.5	1729	2	O9U617_DROME
14	1230.5	29.5	907	2	O44359_NBPCL
15	1219.5	29.2	860	2	O8C9L8_MOUSE
16	1218	29.2	860	1	ELN_MOUSE
17	1215	29.1	810	2	O9ES29_MOUSE
18	1195.5	28.6	875	2	O5RKH4_RAT
19	1185	28.4	864	1	ELN_RAT
20	1159	27.8	1071	2	O7YU48_DROME
21	1142	27.4	747	1	ELN_BOVIN
22	1137	27.2	672	1	PHXR3_MOUSE
23	1136	27.2	871	2	O44358_NBPCL
24	1100	26.4	1217	2	O8V1Y9_MYCTU
25	1096	26.3	1901	1	PG54_MYCTU
26	1094.5	26.2	992	2	O7TWB8_MYCBO
27	1089.5	26.1	1079	2	O6MMW7_MYCTU
28	1087	26.0	1938	2	O7TWC0_MYCBO
29	1084	26.0	1715	2	O8V1Z0_MYCTU
30	1077	25.8	1489	2	O6MMW6_MYCTU
31	1077	25.8	1460	2	O7TWC3_MYCBO

32	1064	25.5	1468	2	O9GUB5_GALME	O9gub5 galleria me
33	1058.5	25.4	786	1	ELN_HUMAN	PL1502 homo saplen
34	1041	24.9	747	1	SPDI_NBPCL	PI19837 nephila cia
35	1034	24.8	1660	2	O79FD4_MYCTU	O79fd4 mycobacteri
36	1034	24.8	1665	2	O7D721_MYCTU	O7d721 mycobacteri
37	1019	24.4	651	2	O9BI09_ARGTR	O9biu9 argiope tri
38	1017.5	24.4	854	2	O9BI04_DOLTE	O9biu4 dolomades t
39	1010.5	24.2	1329	2	O79FP2_MYCTU	O79fp2 mycobacteri
40	1007.5	24.1	1408	2	O8VK17_MYCTU	O8vk17 mycobacteri
41	1007	24.1	1408	2	O7U022_MYCBO	O7u022 mycobacteri
42	1006	24.1	1381	2	O6MMW9_MYCTU	O6mmw9 mycobacteri
43	1003	24.0	1384	2	O8V1Z1_MYCTU	O8v1z1 mycobacteri
44	998.5	23.9	1274	2	O6CHN8_YARLI	O6chn8 yarrowia li
45	992	23.8	1360	2	O7TWC4_MYCBO	O7twc4 mycobacteri

ALIGNMENTS

RESULT 1

ID	FIBH_BOMMO	STANDARD	PRT	5263 AA.
AC	P05790; Q17220; Q26379;			
DT	01-NOV-1988 (Ref. 09, Created)			
DT	16-OCT-2001 (Ref. 40, Last sequence update)			
DT	13-SEP-2005 (Ref. 48, Last annotation update)			
DE	Fibroin heavy chain precursor (Fib-H) (H-fibroin).			
GN	Name=FIBH;			
OS	Bombyx mori (Silk moth).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;			
OC	Bombycidae; Bombyx.			
OX	NCBI_TaxID=7091;			
RN	[1]			
RN	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=20330362; PubMed=10871375; DOI=10.1093/nar/28.12.2413;			
RA	Zhou C.-Z., Confalonieri F., Medina N., Zivanovic Y., Esnault C.,			
RA	Yang T., Jacquet M., Jin J., Duguet M., Perras R., Li Z.-G.;			
RT	"Fine organization of Bombyx mori fibroin heavy chain gene.";			
RL	Nucleic Acids Res. 28:2413-2419(2000).			
RN	[2]			
RN	NUCLEOTIDE SEQUENCE OF 1-168.			
RX	MEDLINE=80045039; PubMed=498286; DOI=10.1016/0092-8674(79)90075-8;			
RA	Tajino Y., Suzuki Y.;			
RT	"The DNA sequence of Bombyx mori fibroin gene including the 5'			
RT	flanking, mRNA coding, entire intervening and fibroin protein coding			
RT	regions.";			
RL	Cell 18:591-600(1979).			
RN	[3]			
RN	PARTIAL NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=79211211; PubMed=455439; DOI=10.1016/0092-8674(79)90018-7;			
RA	Tajino Y., Suzuki Y.;			
RT	"Structural analysis of the fibroin gene at the 5' end and its			
RT	surrounding regions.";			
RL	Cell 16:425-436(1979).			
RN	[4]			
RN	PARTIAL NUCLEOTIDE SEQUENCE.			
RX	STRAIN=Kinsu X Showa;			
RC	MEDLINE=89094868; PubMed=3210244;			
RA	Mita K., Ichimura S., Zama M., James T.C.;			
RT	"Specific codon usage pattern and its implications on the secondary			
RT	structure of silk fibroin mRNA.";			
RL	J. Mol. Biol. 203:917-925(1988).			
RN	[5]			
RN	PARTIAL NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=94365842; PubMed=7916056; DOI=10.1007/BF00175878;			
RA	Mita K., Ichimura S., James T.C.;			
RT	"Highly repetitive structure and its organization of the silk fibroin			
RT	gene.";			
RL	J. Mol. Evol. 38:583-592(1994).			
RN	[6]			
RN	NUCLEOTIDE SEQUENCE OF 5179-5263, AND DISULFIDE BONDS.			
RC	STRAIN=J-139,			

RX MEDLINE=99296390; PubMed=10366732; DOI=10.1016/S0167-4838(99)00088-6;
RA Tanaka K., Kajiyama N., Ishikura K., Waga S., Kikuchi A., Ohtomo K.,
RA Takagi T., Mizuno S.;
RT "Determination of the site of disulfide linkage between heavy and
RT light chains of silk fibroin produced by Bombyx mori.";
RL Biochim. Biophys. Acta 1432:92-103(1999).
RN [17]
RP PARTIAL NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Daizo;
RX PubMed=15591204; DOI=10.1126/science.1102210;
RA Xia Q., Zhou Z., Lu C., Cheng D., Dai F., Li B., Zhao P., Zha X.,
RA Cheng T., Chai C., Pan G., Xu J., Liu C., Lin Y., Qian J., Hou Y.,
RA Wu Z., Li G., Pan M., Li C., Shen Y., Lan X., Yuan L., Li T., Xu H.,
RA Yang G., Wan Y., Zhu Y., Yu M., Shen W., Wu D., Xiang Z., Yu J.,
RA Wang J., Li R., Shi J., Li H., Li G., Su J., Wang X., Li G., Zhang Z.,
RA Wu Q., Li J., Zhang Q., Wei N., Xu J., Sun H., Dong L., Liu D.,
RA Zhao S., Zhao X., Meng Q., Lan F., Huang X., Li Y., Fang L., Li C.,
RA Li D., Sun Y., Zhang Z., Yang Z., Huang Y., Xi Y., Qi Q., He D.,
RA Huang H., Zhang X., Wang Z., Li W., Cao Y., Yu Y., Yu H., Li J.,
RA Ye J., Chen H., Zhou Y., Liu B., Wang J., Ye J., Ji H., Li S., Ni P.,
RA Zhang J., Zhang Y., Zheng H., Mao B., Wang W., Ye C., Li S., Wang J.,
RA Wong G.K.-S., Yang H.;
RT "A draft sequence for the genome of the domesticated silkworm (Bombyx
RT mori).";
RL Science 306:1937-1940(2004).
RN [8]
RP SUBUNIT.
RX MEDLINE=20568317; PubMed=10986287; DOI=10.1074/jbc.M006897200;
RA Inoue S., Tanaka K., Ariaka F., Kimura S., Ohtomo K., Mizuno S.;
RT "Silk fibroin of Bombyx mori is secreted, assembling a high molecular
RT mass elementary unit consisting of H-chain, L-chain, and p25, with a
RT 6:6:1 molar ratio.";
RL J. Biol. Chem. 273:40517-40528(2000).
CC -1- FUNCTION: Core component of the silk filament; a strong, insoluble
CC and chemically inert fiber.
CC -1- SUBUNIT: Silk fibroin elementary unit consists in a disulfide-
CC linked heavy and light chain and a p25 glycoprotein in molar
CC ratios of 6:6:1. This results in a complex of approximately 2.3
CC MDA.
CC -1- TISSUE SPECIFICITY: Produced exclusively in the posterior (PSC)
CC section of silk glands, which are essentially modified salivary
CC glands.
CC -1- DOMAIN: Composed of antiparallel beta sheets. The strands of the
CC beta sheets run parallel to the fiber axis. Long stretches of silk
CC fibroin are composed of microcrystalline arrays of (I-Gly-Ser-Gly-
CC Ala-Gly-Ala)-n interrupted by regions containing bulkier residues.
CC The fiber is composed of microcrystalline arrays alternating with
CC amorphous regions.
CC -1- PTM: The interchain disulfide bridge is essential for the
CC intracellular transport and secretion of fibroin.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF226688; AAF6983.1; -; Genomic DNA.
CC EMBL; V00094; CAA2343.1; -; Genomic DNA.
CC EMBL; V00097; CAA2343.1; -; Genomic DNA.
CC EMBL; S74439; AAB3186.1; -; mRNA.
CC EMBL; X13863; CAA32076.1; -; mRNA.
CC EMBL; M35378; AAA27839.1; -; mRNA.
CC EMBL; AB017362; BAA33147.1; -; genomic DNA.
CC EMBL; C538369; -; NOT ANNOTATED CDS; mRNA.
CC EMBL; AADK0100575; -; NOT ANNOTATED CDS; Genomic DNA.
CC PIR; S01844; S01844.
CC Repeat; Signal; Silk.
CC SIGNAL 1 21
CC CHAIN 22 5263
CC REGION 149 5206
CC DISUFID 5244 5244
CC FT 5260 5263
CC DISUFID 5260 5263
CC Potential.
CC Fibroin heavy chain.
CC Highly repetitive.
CC Interchain (with C-190 in light chain).

FT CONFLICT 10 10 C -> V (in Ref. 2).
SQ SEQUENCE 5263 AA; 391593 MM; 8EE1D3A0A47440E CRC64;
Query Match 50.5%; Score 2107.5; DB 1; Length 5263;
Best Local Similarity 56.2%; Pred. No. 1,8e-118;
Matches 509; Conservative 6; Mismatches 234; Indels 157; Gaps 36;
QY 1 GAGAGSAGAGSGVGV---PGVGV-----PGVGPVGKGVPGVGPVGPVGPVGP 48
DB 2655 GAGAGSGAGAGSGAGAGTGAAGVGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGS 2714
QY 49 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS 108
DB 2715 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS 2772
QY 109 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS 152
DB 2773 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS 2832
QY 153 GVGPGVPGVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPV 202
DB 2833 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGTGV 2892
QY 203 -----GVGVPGKGVPGVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPV 254
DB 2893 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS 2952
QY 255 GVGPGVPGVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPV 311
DB 2953 GA-GYGA-GVGA-GYGVGYGAGAGAGYGAAGAGAGAGAGAGAGAGAGAGAGAGAG 3009
QY 312 SGVGV- PGVGVPGVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPV 363
DB 3010 SGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS 3069
QY 364 AGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 402
DB 3070 AGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 3128
QY 403 GPGVPGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 456
DB 3129 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGV- GYGA 3186
QY 457 GVGPGVPGVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGP 516
DB 3187 GAGAGTGAAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 3244
QY 517 GVGPGVGP-----GVGPAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 551
DB 3245 GAGAGTSSSGFPGPYVANGVSGVGYEYVMSSESDTGTSGAGAGSGAGAGSGAGAGSGAGAG 3304
QY 552 SGVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGP 611
DB 3305 SGAGA-----GYGA-----GVGAGTGAAGAGSGAGAGSGAGAGSGAGAGSGAGAG 3352
QY 612 SGVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGP 671
DB 3353 SGAGA-GYGA-GAG-----SGTGSAGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 3404
QY 672 SGVGPV- GVGVPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPV 727
DB 3405 SGVGAAGTGVGTGAAGAGAGTGVGTGAAGAGAGTGAAGAGAGTGAAGAGAGAGAGAGAGAGAG 3464
QY 728 AGAGSGVGV-----PGVGV---PGVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPVGPV 774
DB 3465 AGAGSGAGAGSGAGAGSGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGS 3523
QY 775 GAGAGS 780
DB 3524 GAGAGS 3529
RESULT 2

06Q294	AGEAP
ID	Q6Q294_AGEAP PRELIMINARY; PRT; 897 AA.
AC	Q6Q294;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Major amputillate spideroin (Fragment).
OS	Agelenopsis aperta (Funnel-web spider).
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC	Araneomorphae; Entelegynae; Agelenidae; Agelenopsis.
OX	[1] NCBI_TaxId=6908;
RN	
RP	NUCLEOTIDE SEQUENCE.
RA	Tian M.; Liu C.; Lewis R.;
RT	"Analysis of Major Amputillate Silk CDNA's from Two Non-Ord-weaving
RT	Spiders";
RL	Biomacromolecules 0:0-0(2004) .
DR	EMBL; AY566305; AAT08436.1; -; mRNA.
FT	NON_TER 1
SQ	SEQUENCE 897 AA; 70174 MW; FA/663A8E802E60 CRC64;

Query Match	45.9%;	Score 1916.5;	DB 2;	Length 897;
Best Local Similarity	50.8%;	Pred. No. 1.4e-107;		
Matches 435; Conservative	66;	Mismatches 207;	Indels 149;	Gaps 31

[illegible]

Oy	66	GAAAGSGGVCVPGVGVPGVGVPKGVPGVGPVGVGGVGVPPAGAASGA-----	716
Db	656	GACAGCGAGIGRLTG-SGLGA--GSGR-GAAGAGSSGAGAGAGAGSGSGAGAGLGLG	712.2
Oy	717	-----GAGSAGAGSGAGAGSGGVCV-PCVGPVGVGVPEKGV-PCVGPVGVGGV	763
Dd	713	LQAGLVSVGTGTGAKAGAGSGAGAGSGAGAGPCTGYATTAATYASSSTGCPGVSGAGAGSG	772
Oy	764	PGVPGAGAGSGAGAGS	780
Dd	773	SGAGSAAGAGSGSGAGA	789

RESULT 3
Q6PY84 KUKHI
ID Q6PY84_KUKHI PRELIMINARY; PRT; 760 AA

DT	05-JUL-2004	(TREMBlrel. 27, Created)
DT	05-JUL-2004	(TREMBlrel. 27, last sequence update)
DT	05-JUL-2004	(TREMBlrel. 27, last annotation update)

05 *Kukulcania hibernalis* (Southern house spider).
0C Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
0C Araneomorphae; Haplogynae; Filistatidae; Kukulcania.

RT "Analysis of Major Ampullate Silk cDNAs from Two Non-Orb-Weaving
RT Spiders";
RT Biomacromolecules 0:0-0(2004).
DR EMBL; AY571308; AA708433.1; -; mRNA.

SEQUENCE 760 AA; 59989 MW; D98439784D9A2A8D CRC64

Query Match	36.7%;	Score 1531;	DB 2;	Length 760;
Best Local Similarity	46.3%;	Pred. No. 1.5e-84;		
Matches 401; Conservative	37;	Mismatches 224;	Indels 204;	Gaps 33

2 AGAGSGAGAGSGVPGVGVPgKGVPGVGPGVGPGVGPGAGAGSGAGAGSG 61

Db 11 ASMAAAGAGSGRRPG-----GARSRGAGAGAGAGAGG 63
Qy 62 AGA-----GAGAGAGSGVGPVGVPKG-----VPGVPGVPG 101

D5 64 AGCEGGFEECGGYAGAGAGAGYAGAG--GRGCGCGGGAATSSASSASVATVESAGAGAG 122

Dd 122 AGTGVGAGAGAGAGAGTGGAGAGAGSAGAGCYAGTAG---GRGRGRGRGEATFSASSASLS 177

Qy 151 ---VPGVGPPG-VGPVGPGAGAGSGAGAGSG-----AGAGSGAGAGSGVGV 196

D5 178 AAVFESAGCELEAGSSGDDAASAAASAAAAAGAGSCNRGPGCARSRGAGAGAGAGAGSCTGG 237

Dd 238 YGSG-SSGA-----GAGAGAGAGGEGCGTGGCGGTGAGAGAGGSSGAGAGAGSSGA 290

Oy 257 PGVGPVGVPVPGKGVPGVGPVGPBGVGPVGPVPGAGAGSAGAAGSAGAGAGSCVGV 316

Dd 291 -----GEGV-GSGAGAGAGAGTGTGAGAGAGAGAGCGSSGAGAGAGTGTGTG 338

D5 339 AG----GCGRCGCGCEAFSSASSSAAVVFESAGPDEEAGSSGGGASAAAAAAGAGSG 394

D5 395 RRRPGGASRGGAGAGAGSGVCGYGSQ--SAGAA-----GAGAGAGACGEAGCFBGGQG 447

DY 412 AGSGAGAGSGAGAAGAGAGSGVGVPGVGVPGKGVPGVPGVPGVPGVPGAG 471

[illegible]

AC O8C918;
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
 DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
 DE library, clone:A630042119 product:elastin, full insert sequence
 DE (Elastin).
 GN Name=ElN;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl J., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L. M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barth G.,
 RA Blake J., Bonfelli D., Bojunga N., Carninci P., de Bonaldo M. F.,
 RA Brownstein M. J., Bult C., Fletcher C., Fujita M., Gariboldi M. F.,
 RA Guncionich S., Hill D. P., Bult C., Hume D. A., Kamaya M., Lee N. H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monacets P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K. H., Weltz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Thymus;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osaio N., Saito R., Suzuki H., Yamana K. I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D. P., Bult C., Hume D. A., Quackenbush J.,
 RA Schirml L. M., Knapin A., Matsuda H., Batalov S., Beisel K. W.,
 RA Blake J. A., Bird T., Brusic V., Choithia C., Corbani L. E., Cousins S.,
 RA Dalia E., Dragani T. A., Fletcher C. F., Forrest A., Frazer K. S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough U.,
 RA Grimmond S., Guncionich S., Hirokawa N., Jackson I. D., Jarvis E. D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R. M., King B. L.,
 RA Konoaga A. A., Kurochkin I. V., Lee Y., Lenhard B., Lyons P. A.,
 RA Maglott D. R., Malais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagahima T., Numata K., Okido T., Pavan W. J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J. O., Qi D., Ramachandran S.,
 RA Ravaei T., Reed J. C., Reed D. J., Reid J., Ring B. Z., Ringwald M.,
 RA Savelin A., Schneider C., Semple C. A., Setou M., Shimada K.,
 RA Sultana R., Takekura Y., Taylor M. S., Teasdale R. D., Tomita M.,
 RA Verrardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L. G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirose-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E. S., Rogers J.,

RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 50,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitanai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsuno H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R. L., Collins F. S., Wagner L., Shennan C. M., Schuler G. D.,
 RA Altschul S. F., Zeeberg B., Buetow K. H., Schaefer C. F., Bhat N. K.,
 RA Hopkins R. F., Jordan H., Moore T., Wax S. T., Wang J., Heien F.,
 RA Datchenko L., Marusina K., Farmer A. A., Rubin G. M., Hong L.,
 RA Scapleton M., Soares M. B., Bonaldo M. F., Casavant T. J., Scheetz T. E.,
 RA Brownstein M. J., Uddin T. B., Tohyuki S., Carninci P., Prange C.,
 RA Raba S. S., Longellano N. A., Peters G. J., Abramson R. D., Mullaly S. J.,
 RA Bosak S. A., McEwan P. J., McKernan K. J., Malek J. A., Gunaratne P. H.,
 RA Richards S., Worley K. C., Hale S., Garcia A. M., Gay L. V., Huily S. W.,
 RA Villalón D. R., Muzny D. M., Sodergren E. J., Lu X., Gibbs R. A.,
 RA Fahney J., Halton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A. C., Shevchenko Y., Bouffard G. G.,
 RA Blakesley R. W., Touchman J. W., Green E. D., Dickson M. C.,
 RA Rodriguez A. C., Grimwood J., Schmutz J., Myers R. M.,
 RA Butterfield Y. S. N., Krzywicki M. I., Skalska U., Smellie D. E.,
 RA Schnerch A., Schein J. E., Jones S. J. M., Marra M. A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RX Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AK041860; BAC31084.1; -, mRNA.
 DR EMBL; BC051649; AA051649.1; -, mRNA.

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OM protein - protein search, using sw model

Run on: May 10, 2006, 10:36:19 ; Search time 189 Seconds
(Without alignments)
1813.309 Million cell updates/sec

Title: US-10-800-179-19

Perfect score: 4173
Sequence: 1 GAAGAGGAGAGGAGVPGVG.....GVGPGVPGAGAGAGAGS 780

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseqp21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4173	100.0	780	ADK51951	ADK51951 Repeat pr
2	4173	100.0	780	ADR70468	ADR70468 Silk-el
3	4173	100.0	780	ADU98730	ADU98730 Active ag
4	4173	100.0	780	ADU81661	ADU81661 Silk-el
5	4173	100.0	780	ABE57376	ABE57376 SEIP 47K
6	3448	82.6	884	AAR80341	AAR80341 Protein p
7	3448	82.6	884	AAW09213	AAW09213 SEIP8K po
8	3448	82.6	884	AAW53541	AAW53541 Expected
9	3448	82.6	884	AAW49728	AAW49728 SEIP8K po
10	3448	82.6	884	AAV51882	AAV51882 Plasmid p
11	3448	82.6	884	ABG31412	ABG31412 SEIP8K po
12	3448	82.6	884	ABW01628	ABW01628 Plasmid p
13	3448	82.6	884	ADR70473	ADR70473 Silk-el
14	3448	82.6	884	ADU98735	ADU98735 Active ag
15	3448	82.6	884	ADU81666	ADU81666 Silk-el
16	3448	82.6	884	ABE57381	ABE57381 SEIP 47E-
17	3448	82.6	983	ADU81678	ADU81678 Cordon bi
18	3448	82.6	1027	ADU81673	ADU81673 Cecropin
19	3448	82.6	1105	ADU81674	ADU81674 Antimicro
20	3448	82.6	1125	ADU81675	ADU81675 Green flu
21	3346	80.2	965	ADU81679	ADU81679 Active ag
22	3346	80.2	965	ADU98741	ADU98741 Active ag
23	3346	80.2	965	ADU81672	ADU81672 Silk/el
24	3346	80.2	965	ABE57387	ABE57387 SEIP 58 r

25	3305	79.2	1038	8	ADR70478	ADR70478 Silk-el
26	3305	79.2	1038	9	ADU98740	ADU98740 Active ag
27	3305	79.2	1038	9	ADU81671	ADU81671 Silk/el
28	3305	79.2	1038	9	ABE57386	ABE57386 SEIP 67K
29	3296	79.0	2257	1	AAAP82961	AAAP82961 SEIP3 pro
30	3296	79.0	2257	2	AAAR41012	AAAR41012 SEIP3 mul
31	3296	79.0	2257	2	AAW26347	AAW26347 SEIP3 syn
32	3296	79.0	2257	3	AAW53523	AAW53523 Amino aci
33	3296	79.0	2257	3	AAV78282	AAV78282 SEIP3 ami
34	3296	79.0	2257	5	ABG69272	ABG69272 Silk/el
35	3296	79.0	2257	7	ADBE4977	ADBE4977 Recombina
36	3284	78.7	877	2	AAAR80335	AAAR80335 Protein p
37	3284	78.7	877	2	AAW49724	AAW49724 Protein p
38	3264	78.2	768	5	ABP53466	ABP53466 SEIP8 rel
39	3263	78.2	1016	9	ADU81677	ADU81677 Radioprot
40	3263	78.2	1016	9	ABE57388	ABE57388 SEIP47K-P
41	3253	78.0	832	2	AAAR80252	AAAR80252 Polymer S
42	3253	78.0	832	5	ABP53473	ABP53473 Protein p
43	3250	77.9	1043	9	ADU81676	ADU81676 Cordon bi
44	3192	76.5	768	5	ABP53481	ABP53481 Protein p
45	3182	76.3	988	2	AAAR80253	AAAR80253 Polymer S

ALIGNMENTS

RESULT 1
ADK51951
ID ADK51951 standard; protein; 780 AA.

AC ADK51951;

DT 06-MAY-2004 (first entry)

DE Repeat protein polymer repeat sequence, SEQ ID 19.

KM repeat protein.

OS unidentified.

PN MO2003099465-A1.

PD 04-DEC-2003.

PF 20-MAY-2003; 2003MO-US015757.

PR 20-MAY-2002; 2002US-0381913P.

PA (DOMO) DOM CORNING CORP.

PI (GENV) GENENCOR INT INC.

Kumar M;

WPI; 2004-023263/02.

Forming inorganic structure, for use as e.g. electronic photonic and nano
composite materials, comprises providing substrate with repeat protein
polymer, and exposing substrate to precursor containing inorganic
species.

Claim 12; Page 8; 27pp; English.

The present invention relates to a method for forming an inorganic
structure. The method comprises providing substrate with a repeat protein
polymer, and exposing the substrate to a precursor comprising inorganic
species. The repeat protein polymer catalyzes the formation of an
inorganic structure on the substrate. The repeat portion of the repeat
protein polymer may be ADK51951-ADK51957, which may have a head sequence
at the N-terminal end (ADK51958) and a tail sequence at the C-terminal
end. (ADK51959-ADK51966).

Sequence 780 AA;

Query Match 100.0%; Score 4173; DB 8; Length 780;
Best Local Similarity 100.0%; Pred. No. 4.4e-264;
Matches 780; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 60
1 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 60
DB 1 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 60
QY 61 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 120
61 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 120
DB 61 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 120
QY 121 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 180
121 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 180
DB 121 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 180
QY 181 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 240
181 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 240
DB 181 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 240
QY 241 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 300
241 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 300
DB 241 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 300
QY 301 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 360
301 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 360
DB 301 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 360
QY 361 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 420
361 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 420
DB 361 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 420
QY 421 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 480
421 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 480
DB 421 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 480
QY 481 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 540
481 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 540
DB 481 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 540
QY 541 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 600
541 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 600
DB 541 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 600
QY 601 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 660
601 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 660
DB 601 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 660
QY 661 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 720
661 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 720
DB 661 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 720
QY 721 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 780
721 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 780
DB 721 GAGAGSAGAGSGSVGPVGVPVGKGVPGKGVPGVGPBGVPGVPGAGSAGAGS 780

RESULT 2
ADR70468
ID ADR70468 standard; protein; 780 AA.
XX ADR70468;
AC
XX
XX 02-DEC-2004 (first entry)
XX
XX Silk-elastin polymer SELP47K.
XX
XX personal care composition; repeat sequence protein polymer;
XX hair care composition; shampoo; conditioner; anti-dandruff treatment;
XX styling aid; styling conditioner; hair repair treatment;
XX chemical hair treatment; hair dye; skin care composition; body wash;
XX antimicrobial cleanser; skin protectant cream; body lotion; facial cream;
XX moisturising cream; facial cleansing emulsion;

KM surfactant-based facial cleanser; facial exfoliating gel;
KM anti-acne treatment; facial toner; exfoliating cream; facial mask;
KM after shave balm; sunscreen; anti-fungal treatment; skin protectant;
KM antiperspirant; cosmetic composition; makeup; eye gel;
KM high-melting point lipstick; lipstick; lip gloss; lip balm; mascara;
KM eyeliner; pressed powder formulation; foundation; nail care composition;
KM nail enamel; cuticle treatment; nail polish; nail treatment;
KM polish remover; oral care composition; toothpaste; mouth rinse;
KM breath freshener; teeth whitening treatment; transparent film formation;
KM over-the-counter pharmaceutical composition; lubricant; softness;
KM hydrogel formation; water-solubility; lubricant; softness;
KM moisture retainer; tensile property; viscoelastic behaviour;
KM glass transition temperature; cloud temperature;
KM decomposition temperature; silk; elastin; repeating sequence unit.

XX Synthetic.
OS
XX
XX US2004180027-A1.
PN
XX
XX 16-SEP-2004.
PD
XX
XX 12-MAR-2004; 2004US-00800179.
PR
XX
XX 12-MAR-2003; 2003US-0454077P.
PA
XX
XX (KUMA/) KUMAR M.
PA (CUER/) CUERAS W A.
XX
XX Kumar M, Cuevas WA;
PI
XX
XX WPI; 2004-675584/66.
DR
XX
XX
PT Personal care composition useful as cosmetic, hair care or skin care
PT product, comprises repeat sequence protein polymer and compounds such as
PT carriers, excipients, liposomes, active ingredients, or emollients.

XX
XX Example 1; SEQ ID NO 19; 50bp; English.
PS
XX
XX The invention describes a personal care composition (i) comprising a
CC repeat sequence protein polymer with the balance of the composition
CC comprising one or more compounds chosen from carriers, excipients,
CC liposomes, active ingredients, biological or botanical products,
CC humectants, emollients, surfactants, thickening agents, silicone
CC components, organic sunscreens, preservatives, neutralising agents,
CC perfumes and pigments. (i) is useful as a hair care composition such as
CC shampoo, conditioner, anti-dandruff treatment, styling aids, styling
CC conditioner, hair repair or treatment, serum, lotion, cream, pomade, or
CC chemical treatment such as hair dye; skin care composition such as
CC moisturising body wash, body wash, antimicrobial cleanser, skin
CC protectant cream, body lotion, facial cream, moisturising cream, facial
CC cleansing emulsion, surfactant-based facial cleanser, facial exfoliating
CC gel, anti-acne treatment, facial toner, exfoliating cream, facial mask,
CC after shave balm or sunscreen; skin care composition topically applied
CC over-the-counter drugs comprising anti-fungal treatments, anti-acne
CC treatments, skin protectants, and antiperspirants; cosmetic composition
CC comprising a makeup composition chosen from eye gel, high-melting point
CC lipstick, lipstick, lip gloss, lip balm, mascara, eyeliner, pressed
CC powder formulation and foundation; nail care composition such as nail
CC enamel, cuticle treatment, nail polish, nail treatment, or polish remover
CC ; an oral care composition such as toothpaste, mouth rinse, breath
CC freshener, or whitening treatment; and over-the-counter pharmaceutical
CC composition. The cosmetic composition is a mascara such as non-waterproof
CC mascara, waterproof mascara, volumising mascara, lengthening mascara,
CC curling mascara, anhydrous waterproof mascara, water-based mascara, or
CC eyelash or eyebrow treatment; a pressed powder formulation such as loose
CC powder, blush, eye shadow, or bronzing powder; foundation such as water-
CC in-oil foundation, water-in-silicone foundation, oil-in-water foundation,
CC anhydrous makeup stick, or cream-to-powder foundation. (i) has desired
CC characteristics such as transparent film formation, hydrogel formation,
CC better efficacy and binding to skin, hair, nail, and oral surfaces,
CC desired level of hydrophobicity with water-solubility, imparting lubricant,
CC softness, moisture retainer, and mechanical properties (such as tensile
CC properties, viscoelastic behaviour, glass transition temperature, cloud

CC temperature and decomposition temperature), and does not have any
CC chemical modifications of the protein. This is the amino acid sequence of
CC silk-elastin polymer SELP47K that may be used as the repeat sequence
CC protein polymer of the invention.

XX Sequence 780 AA;

Query Match 100.0%; Score 4173; DB 8; Length 780;
Best Local Similarity 100.0%; Pred. No. 4,4e-264;
Matches 780; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 60
DB 1 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 60
QY 61 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 120
DB 61 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 120
QY 121 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 180
DB 121 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 180
QY 181 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 240
DB 181 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 240
QY 241 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 300
DB 241 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 300
QY 301 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 360
DB 301 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 360
QY 361 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 420
DB 361 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 420
QY 421 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 480
DB 421 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 480
QY 481 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 540
DB 481 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 540
QY 541 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 600
DB 541 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 600
QY 601 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 660
DB 601 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 660
QY 661 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 720
DB 661 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 720
QY 721 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 780
DB 721 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 780

RESULT 3
ADU98730 ID ADU98730 standard; protein; 780 AA.

AC ADU98730;
XX 10-FEB-2005 (first entry)
XX Active agent release control system-related SELP47K protein SeqId19.
DB

XX cosmetics; delivery mechanism; SELP47K.
XX Unidentified.
OS US2004228913-A1.
XX 18-NOV-2004.
XX 14-MAY-2004; 2004US-00845775.
XX 14-MAY-2003; 2003US-0470465P.
XX

PA (KUMAR/) KUMAR M.
PA (MAZE/) MAZEAUD I.
PA (CHRISTIANO/) CHRISTIANO S P.
PI Kumar M, Mazeaud I, Christiano SP;
XX WPI: 2005-037015/04.
DR

PT System for providing controlled release delivery of active agent useful
PT for incorporating active agents into personal care product compositions,
PT comprises repeat sequence protein polymer and active agent.

PS Claim 12; SEQ ID NO 19; 34pp; English.

CC This invention relates to a novel system for providing controlled release
CC delivery of an active agent which comprises a repeat sequence protein
CC polymer and at least one active agent. The invention may be useful in a
CC hair care composition, skin care composition, nail care composition,
CC cosmetic composition, oral care composition or over-the-counter
CC pharmaceutical composition. The system may be useful in shampoos, gels,
CC mousses and other hair care products, rinse-off conditioners, skin care
CC products such as moisturizers, toners and makeup and nail care products
CC such as polishes and polish removers. The invention enables controlled
CC release of active agents. The present sequence is that of an SELP47K
CC protein which may be used in the system of the invention.

XX Sequence 780 AA;

Query Match 100.0%; Score 4173; DB 9; Length 780;
Best Local Similarity 100.0%; Pred. No. 4,4e-264;
Matches 780; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 60
DB 1 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 60
QY 61 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 120
DB 61 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 120
QY 121 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 180
DB 121 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 180
QY 181 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 240
DB 181 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 240
QY 241 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 300
DB 241 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 300
QY 301 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 360
DB 301 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 360
QY 361 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 420
DB 361 GAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGVGPVGVPVGVPVGPGVPGAGAGSGAGAGS 420

Qy	421	GAGAGSGAGAGSGVGPVGVPBGVGPBGKGVGPBGVGPBGVGPBGVGPBGAGSGAGAGS	480
Db	421	GAGAGSGAGAGSGVGPVGVPBGVGPBGKGVGPBGVGPBGVGPBGVGPBGAGSGAGAGS	480
Qy	481	GAGAGSGAGAGSGVGPVGVPBGVGPBGKGVGPBGVGPBGVGPBGVGPBGAGSGAGAGS	540
Db	481	GAGAGSGAGAGSGVGPVGVPBGVGPBGKGVGPBGVGPBGVGPBGVGPBGAGSGAGAGS	540
Qy	541	GAGAGSGAGAGSGVGPVGVPBGVGPBGKGVGPBGVGPBGVGPBGVGPBGAGSGAGAGS	600
Db	541	GAGAGSGAGAGSGVGPVGVPBGVGPBGKGVGPBGVGPBGVGPBGVGPBGAGSGAGAGS	600
Qy	601	GAGAGSGAGAGSGVGPVGVPBGVGPBGKGVGPBGVGPBGVGPBGVGPBGAGSGAGAGS	660
Db	601	GAGAGSGAGAGSGVGPVGVPBGVGPBGKGVGPBGVGPBGVGPBGVGPBGAGSGAGAGS	660
Qy	661	GAGAGSGAGAGSGVGPVGVPBGVGPBGKGVGPBGVGPBGVGPBGVGPBGAGSGAGAGS	720
Db	661	GAGAGSGAGAGSGVGPVGVPBGVGPBGKGVGPBGVGPBGVGPBGVGPBGAGSGAGAGS	720
Qy	721	GAGAGSGAGAGSGVGPVGVPBGVGPBGKGVGPBGVGPBGVGPBGVGPBGAGSGAGAGS	780
Db	721	GAGAGSGAGAGSGVGPVGVPBGVGPBGKGVGPBGVGPBGVGPBGVGPBGAGSGAGAGS	780

RESULT 4

ID ADU81661 standard; protein; 780 AA.

AC ADU81661;

DT 10-FEB-2005 (first entry)

DE Silk-elastin polymer SLP47K, SEQ ID NO:19.

KW Protein engineering; protein stabilization; cosmetics; textile; filter;

KW fibroin; elastin.

OS Bombyx mori

OS Chimeric.

XX

XX

XXXXXX

XX

XX

PA (CUEV/) CUEVAS W A.

XX

XX

✕

PT composition, cosmetic, oral care composition, comprising conjugation

XX

XX

CC sequence protein polymer (i.e., an engineered protein) and at least

CC sunscreens, lanolin, vitamins, bleaches, thickening agents,

CC protein polymer preferably comprises a repeating amino acid sequence unit

CC dragline silk, gluten high molecular subunit, titin, fibronectin,

CC	lentinan, llaudin, glue polypeptide, ice nucleating protein, keratin,
CC	mucin, RNA polymerase II, resilin or mixtures thereof. The repeat
CC	sequence protein polymers provide a scaffolding to which active agents
CC	may be bound. In particular, they enhance the ability to utilize proteins
CC	and peptides as active agents as they overcome many of the
CC	hydrophobicity, solubility, and binding limitations associated with
CC	polypeptide active agents, and allow the use of polypeptide active agents
CC	in applications for which a total protein environment is desirable. The
CC	invention also relates to personal care compositions comprising a
CC	biomolecular conjugate of the invention, a method of making the personal
CC	care compositions; a method of making a biomolecular conjugate by
CC	recombinantly producing a fusion protein comprising the repeat sequence
CC	protein polymer and a polypeptide active agent; biomaterials adapted for
CC	at least one predetermined desirable function which comprise one or more
CC	biomolecular conjugates comprising a silk elastin polymer as the repeat
CC	sequence protein polymer and a polypeptide active agent; and a method of
CC	producing such biomaterials. The biomolecular conjugates are useful in
CC	personal care compositions such as over-the-counter pharmaceutical
CC	compositions, and compositions used for hair care, skin care, nail care,
CC	oral care and cosmetics. The biomolecular conjugates are also useful in
CC	biomaterials such as textiles (e.g., protective garments), filters,
CC	creams, coatings, and dressings, and in biomaterials useful in genetics
CC	research tools or in search and/or identification tools. The present
CC	sequence represents silk-elastin polymer SEBP47K, a repeat sequence
CC	protein polymer comprising silk fibroin and elastin repeat sequences
CC	which is specifically claimed for use in biomolecular conjugates of the
CC	invention.
XX	
SO	Sequence 780 AA;
Query Match	100.0%; Score 4173; DB 9; Length 780;
Best Local Similarity	100.0%; Prid. NO. 4,4e-264;
Matches 780; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

SQ Sequence 780 AA;

Query Match 100.0%; Score 4173; DB 9; Length 780;

Matches 780; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]


```
RESULT 6
AAR80341
ID AAR80341 standard; protein; 884 AA.
XX
AC AAR80341;
XX
DT 18-APR-1996 (first entry)
XX
DE Protein polymer adhesive substrate SELP8K.
XX
KW Pendent group; repeating unit; enzyme recognition site; sealant; fibrin;
KM enzymatic cross-linking; biocompatible material; structural integrity;
KM medical adhesive; wound closure; tissue repair; transglutaminase.
XX
OS Synthetic.
XX
PN MO9523611-A1.
XX
PD 08-SEP-1995.
XX
PF 03-MAR-1995; 95MO-US002728.
XX
PR 03-MAR-1994; 94US-00205518.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
XX
PI Cappello J;
XX
DR WPI; 1995-320413/41.
XX
PT Protein polymers comprising repeating units and sequences - capable of
PT enzymatic catalyzed covalent bond formation useful as a biocompatible
PT material for wound closure and tissue repair.
XX
PS Example 7; Page 65; 138pp; English.
XX
CC The sequence of the protein polymer adhesion substrate (PPAS) SELP8K. The
CC protein contains 12 repeats of the SELP8K monomer sequence (AAR80339).
CC The protein can be used as a polymer substrate in an isopeptide cross-
CC linking reaction catalysed by a transglutaminase enzymatic activity, e.g.
CC Factor VIII or XIII. The polymers can be used in biological systems where
CC in situ formation of a biocompatible material with structural integrity
CC is required e.g. as medical adhesives and sealants or for wound closure
CC or tissue repair.
XX
SQ Sequence 884 AA;
XX
Query Match 82.6%; Score 3448; DB 2; Length 884;
Best Local Similarity 90.6%; Pred. No. 6, 9e-217;
Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;
QY 3 GAGSGAGAGSGGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 58
DB 34 GAGSGAGAGSGGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 93
QY 59 GSGAGAGSGAGSGGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGS 114
DB 94 GSGAGAGSGAGSGGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGS 153
QY 115 GAGAGSGAGAGSGAGSGGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGA 170
DB 154 GAGAGSGAGAGSGAGSGGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGA 213
QY 171 GAGSGAGAGSGAGAGSGAGSGGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG 227
DB 214 GAGSGAGAGSGAGAGSGAGSGGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG 273
QY 228 -PGAAGSGAGAGSGAGAGSGAGSGGVPGVPGVPGKGVPGVG-PGVG-PGVG- 283
DB 274 VPAGAGSGAGAGSGAGAGSGAGSGGVPGVPGVPGKGVPGVG-PGVG-PGVG- 333
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QY 284 PGVG-PGAGAGSGAGAGSGAGSGGVPGVPGVPGKGVPGVG-PGVG-P 340
DB 334 PGVPGVPGAGAGSGAGAGSGAGSGGVPGVPGVPGKGVPGVG-PGVG-P 393
QY 341 GVG-PGVG-PGAGAGSGAGAGSGAGSGGVPGVPGVPGKGVPGVG-PG 397
DB 394 GVGPGVPGVPGAGAGSGAGAGSGAGSGGVPGVPGVPGKGVPGVG-PG 453
QY 398 VG-PGVG-PGVG-PGAGAGSGAGAGSGAGSGGVPGVPGVPGKGVPGV 454
DB 454 VGVPGVPGVPGVPGAGAGSGAGAGSGAGSGGVPGVPGVPGVPGVPGK 513
QY 455 G-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGSGGVPGVPGVPGK 510
DB 514 GVPGVPGVPGVPGVPGAGAGSGAGAGSGAGSGGVPGVPGVPGVPGV 573
QY 511 VPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGSGGVPGVPGV 566
DB 574 VPGKGVPGVPGVPGVPGAGAGSGAGAGSGAGSGGVPGVPGVPGV 633
QY 567 PGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGSGGVPGV 622
DB 634 PGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 653
QY 623 GVGVPKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGSGV 678
DB 694 GVGVPVPGVPGKGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 753
QY 679 VGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAG 734
DB 754 VGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 813
QY 735 GVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAG 780
DB 814 GVPGVPGVPGVPGVPGKGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 863

RESULT 7
AAM09213
ID AAM09213 standard; protein; 884 AA.
XX
AC AAM09213;
XX
DT 29-MAR-1997 (first entry)
XX
DE SELP8K polymer.
XX
KW SELP8K; protein polymer; silk; fibroin; elastin; repeat sequence;
KM crosslinking; adhesive; tissue sealant; biocompatible film.
XX
OS Synthetic.
XX
FH Location/Qualifiers
FT Region
FT /note= "Silk fibroin peptide repeat sequence"
FT Peptide
FT /note= "Silk fibroin peptide (AAM09206, claim 4)"
FT Region
FT /note= "Block of 12 identical monomer sequences"
FT Region
FT /note= "Block monomer sequence"
FT Region
FT /note= "Elastin peptide repeat sequence"
FT Peptide
FT /note= "Elastin peptide (AAM09207, claim 4)"
FT Misc-difference
FT /note= "Residue with functional group for crosslinking"
FT Region
FT /note= "Elastin peptide repeat sequence"
FT Region
FT /note= "Silk fibroin peptide repeat sequence"
FT Region
FT /note= "Elastin peptide repeat sequence"
FT Region
FT /note= "Elastin peptide repeat sequence"
```


FT Misc-difference 833 /note= "Residue with functional group for crosslinking"
 FT Region 837..851 /note= "Elastin peptide repeat sequence"
 FT Region 852..863 /note= "Silk fibroin peptide repeat sequence"
 PN MO9634618-A1.
 XX 07-NOV-1996.
 PD 02-MAY-1996; 96WO-US006229.
 XX 05-MAY-1995; 95US-00435641.
 PR (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 PA Stedronsky ER, Cappello J;
 PI WPI; 1996-505895/50.
 XX Tissue repair adhesive comprising polymer of structural protein repeat
 PT units - contg. hetero-atom functional gps. reactive with crosslinking
 PT agent, combines biocompatibility and high bonding strength.
 XX Example 2; Page 25; 103pp; English.
 PS This SELPBK polymer sequence (mol.wt. 69,772) has been constructed from
 CC monomers composed of repeat units derived from silk fibroin (AAM09206)
 CC and elastin (AAM09207) (claim 4). The monomer (AAM09212) has been
 CC amplified by multicopy cloning in Escherichia coli (using plasmid
 CC pPT0345) to produce a recombinant protein polymer backbone with lys
 CC functional groups for subsequent polyfunctional chemical crosslinking.
 CC The crosslinked polymer product forms a strongly adherent tissue adhesive
 CC or sealant. The polymer may be used to seal defects in vessel walls, e.g.
 CC artery, vein, capillary, lung, dura or colon, to increase tissue mass, or
 CC to produce biocompatible films for in vivo use. The sealants have the
 CC biocompatibility of fibrin glues, but set more quickly, and have greater
 CC strength. They are readily prepared by recombinant methods, are easy to
 CC administer, and are gradually resorbed
 CC
 XX Sequence 884 AA:
 SQ
 Query Match 82.6%; Score 3448; DB 2; Length 884;
 Best Local Similarity 90.6%; Pred. No. 6.9e-217;
 Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;

Db 394 GVGVPVPGAGAGSAGAGSAGAGSAGAGSGVGPVGVPVGVPBGKGVPG 453
 Qy VG -PGVG -PGVG -PGAGAGSAGAGSAGAGSAGAGSGVGPVGVPBGKGVPGV 454
 Db 454 VGVPGVPGVGPVPGAGAGSAGAGSAGAGSAGAGSGVGPVGVPBGKGVPGK 513
 Qy 455 G-PGVG -PGVG -PGVG -PGAGAGSAGAGSAGAGSAGAGSGVGPVGVPBGK 510
 Db 514 GVPBGVPGVGPVPGVPGAGAGSAGAGSAGAGSGVGPVGVPBGKGVPGV 573
 Qy 511 VPGVG -PGVG -PGVG -PGAGAGSAGAGSAGAGSAGAGSGVGPVGVPBGV 566
 Db 574 VPGKGVPGVGPVPGVPGAGAGSAGAGSAGAGSGVGPVGVPBGV 633
 Qy 567 PGKGVPGVG -PGVG -PGVG -PGAGAGSAGAGSAGAGSAGAGSGVGPVGP 622
 Db 634 PGVGPBGKGVPGVGPVPGVPGAGAGSAGAGSAGAGSGVGPVGVP 693
 Qy 623 GVGVPBGKGVPGVG -PGVG -PGVG -PGAGAGSAGAGSAGAGSGVGPVG 678
 Db 694 GVGVPBGVPGKGVPGVGPVPGVPGAGAGSAGAGSAGAGSGVGPVG 753
 Qy 679 VGVPGVPGKGVPGVG -PGVG -PGVG -PGAGAGSAGAGSAGAGSGV 734
 Db 754 VGVPGVPGVGPVPGKGVPGVGPVPGVPGAGAGSAGAGSGVGPVG 813
 Qy 735 GVPBGVPGVGPVPGKGVPGVG -PGVG -PGVG -PGAGAGSAGAGS 780
 Db 814 GVPBGVPGVGPVPGVPGKGVPGVGPVPGVPGVPGVPGAGAGSAGAGS 863

RESULT 8
 AAM53541
 ID AAM53541 standard; protein; 884 AA.
 AC AAM53541;
 XX 10-AUG-1998 (first entry)
 DT Expected amino acid sequence of pPT0345 encoding SELPBK polymer.
 DE Polymer SELPBK; peptide repeat unit; DNA repeat unit;
 KW high molecular weight polymer; synthetic silk; silk worm.
 XX Synthetic.
 OS WO9810063-A1.
 FN 12-MAR-1998.
 PD 23-SEP-1996; 96WO-US015306.
 PF 03-SEP-1996; 96US-00707237.
 PR (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 PA Ferrari PA, Cappello J, Crissman JW, Dorman MA;
 PI WPI; 1998-193613/17.
 DR Preparation of synthetic repetitive DNA - useful for construction of
 XX large protein polymers having repeating units, used in structural
 PT material, e.g. synthetic silk.
 PS Example 7; Page 89; 127pp; English.
 XX This is the amino acid sequence of pPT0345 comprising the SELPBK protein,
 CC used in the method of invention, which involves the preparation of
 CC synthetic DNA sequence having repeating units from about 3-15 codons and
 CC encoding a protein of at least about 30 kDa. The method is useful for the
 CC production of high molecular weight polymers (e.g. synthetic silk),
 CC either nucleic acids or peptides that are the expression products of the
 CC nucleic acids and particularly high molecular weight peptides containing

CC	repeating units which are useful structural materials
XX	
XX	Sequence 884 AA:
XX	Query Match 82.6%; Score 3448; DB 2; Length 884;
XX	Best Local Similarity 90.6%; Pred. No. 6.9e-217;
XX	Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;
QY	3 GAGSGAGAGSGVGPVGVPVGKGPVG- -PGVG- -PGVG- -PGVG- -PGAAGSGAGA 58
DB	34 GAGSGAGAGSGVGPVGVPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVG 93
QY	59 GSGAGAGSGAGAGSGVGPVGVPVGKGPVG- -PGVG- -PGVG- -PGVG- -PGAAGS 114
DB	94 GSGAGAGSGAGAGSGVGPVGVPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVG 153
QY	115 GAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVG- -PGVG- -PGVG- -PGA 170
DB	154 GAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVG 213
QY	171 GAGSGAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVG- -PGVG- -PGVG- -PGVG- -PGVG- 227
DB	214 GAGSGAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVG 273
QY	228 -PGAAGSGAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVG- -PGVG- -PGVG- -283
DB	274 VPAGAGSGAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVGKGPVGKGPVGKGPVGKGPVG 333
QY	284 PGVG- -PGAAGSGAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVG- -PGVG- -P 340
DB	334 PGVGVPAGAGSGAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVGKGPVGKGPVGKGPVG 393
QY	341 GVG- -PGVG- -PGAAGSGAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVG- -PG 397
DB	394 GVGVPVGVPAGAGSGAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVGKGPVGKGPVG 453
QY	398 VG- -PGVG- -PGAAGSGAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVG 454
DB	454 VGVPVGVPVGVPAGAGSGAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVGKGPVG 513
QY	455 G- -PGVG- -PGVG- -PGAAGSGAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVG 510
DB	514 GVGVPVGVPVGVPAGAGSGAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVGKGPVG 573
QY	511 VPVG- -PGVG- -PGVG- -PGAAGSGAGAGSGAGAGSGAGAGSGVGPVGVPVG 566
DB	574 VPVGVPVGVPVGVPAGAGSGAGAGSGAGAGSGAGAGSGVGPVGVPVG 633
QY	567 PGKGPVG- -PGVG- -PGVG- -PGAAGSGAGAGSGAGAGSGAGAGSGVGPVGVP 622
DB	634 PGVGVPVGKGPVGVPVGVPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVG 693
QY	623 GVGVPVGKGPVG- -PGVG- -PGVG- -PGAAGSGAGAGSGAGAGSGAGAGSGVGP 678
DB	694 GVGVPVGVPVGKGPVGVPVGVPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVG 753
QY	679 VGVPVGVPVGKGPVG- -PGVG- -PGVG- -PGAAGSGAGAGSGAGAGSGAGAGSGV 734
DB	754 VGVPVGVPVGVPVGKGPVGVPVGVPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVG 813
QY	735 GVGVPVGVPVGKGPVGKGPVG- -PGVG- -PGVG- -PGAAGSGAGAGS 780
DB	814 GVGVPVGVPVGVPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVG 863

RESULT 9
AAW49728 standard; protein; 884 AA.

AAW49728;
AC
XX
DT 25-MAR-2003 (revised)
12-OCT-1998 (first entry)

XX	SELPEK polymer.
DE	
XX	Protein polymer; SELPEK; silk-like protein; fibroin; elastin; adhesive;
KW	sealant; wound healing; transglutaminase; cross-linking.
XX	
XX	Synthetic.
OS	
XX	US5773577-A.
PN	
XX	30-JUN-1998.
PD	
XX	
XX	02-MAR-1995; 95US-00397633.
PF	
XX	03-MAR-1994; 94US-00205518.
PR	
XX	(PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
PA	
PI	Cappello J;
PI	
XX	WPI; 1998-387091/33.
DR	
XX	
XX	New recombinant protein polymers - containing naturally occurring
PT	repetitive units for crosslinking by enzymes, useful as medical adhesives
PT	and sealants, depots and matrices.
PS	
XX	Example 7; Col 43; 70pp; English.
XX	
CC	SELPEK polymer is a synthetic silk-like protein comprising multiple
CC	copies of a monomer (see AAW49726) consisting of repeating units of silk-
CC	like sequences (GAGAS) and elastin-like sequences (VPGVG) including a
CC	reactive lysine residue. It was expressed in Escherichia coli from
CC	plasmid pPT0345 as a 80 kDa protein. The SELPEK polymer was specifically
CC	designed to be functionalised with different reagents reactive to amines.
CC	Claimed recombinant protein polymers are capable of covalent crosslinking
CC	by enzymatic reaction to form products which set quickly and have good
CC	adhesive properties and high strength. The proteins can comprise a
CC	repetitive amino acid backbone of repetitive units having collagen,
CC	fibroin, elastin or keratin motifs and at least 2 enzyme recognition
CC	sequences comprising a glutamine or lysine capable of enzyme catalyzed
CC	isopeptide formation. The products can be used as medical adhesives and
CC	sealants, in the closure of wounds and repair of damaged tissue. (Updated
CC	on 25-MAR-2003 to correct PF field.)
CC	
XX	
XX	
SO	Sequence 884 AA:
QY	Query Match 82.6%; Score 3448; DB 2; Length 884;
DB	Best Local Similarity 90.6%; Pred. No. 6.9e-217;
DB	Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;
QY	3 GAGSGAGAGSGVGPVGVPVGKGPVG- -PGVG- -PGVG- -PGAAGSGAGA 58
DB	34 GAGSGAGAGSGVGPVGVPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVG 93
QY	59 GSGAGAGSGAGAGSGVGPVGVPVGKGPVG- -PGVG- -PGVG- -PGAAGS 114
DB	94 GSGAGAGSGAGAGSGVGPVGVPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVG 153
QY	115 GAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVG- -PGVG- -PGVG- -PGA 170
DB	154 GAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVG 213
QY	171 GAGSGAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVG- -PGVG- -PGVG- -PGVG- -PGVG- 227
DB	214 GAGSGAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVGKGPVGKGPVGKGPVGKGPVGKGPVG 273
QY	228 -PGAAGSGAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVG- -PGVG- -PGVG- -283
DB	274 VPAGAGSGAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVGKGPVGKGPVGKGPVGKGPVG 333
QY	284 PGVG- -PGAAGSGAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVG- -PGVG- -P 340
DB	334 PGVGVPAGAGSGAGAGSGAGAGSGAGAGSGVGPVGVPVGKGPVGKGPVGKGPVGKGPVG 393

QY	341	GVG- -PGVG- -PGAAGSGAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG- -PG	397
Db	394	GVGVGVGVPGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVG- -PGVG- -PGKGVDP	4533
QY	398	VG- -PGVG- -PGVG- -PGAAGSGAGAGSGAGAGSGAGAGSGVGVPGVG- -PGVGVPGKGVPGV	454
Db	454	VGVPGVGVPGVGVPGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVG- -PGVGVPGVGVPGK	513
QY	455	G- -PGVG- -PGVG- -PGVG- -PGAAGSGAGAGSGAGAGSGAGAGSGVGVPGVG- -PGVGVPGK	510
Db	514	GVPGGVGVPGVGVPGVGVPGAGAGSGAGAGSGAGAGSGVGVPGVG- -PGVGVPGVGV	573
QY	511	VPGVG- -PGVG- -PGVG- -PGVG- -PGAAGSGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGV	566
Db	574	VPKGVPGVGVPGVGVPGVGVPGAAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGV	633
QY	567	PGKGVPGVG- -PGVG- -PGVG- -PGVG- -PGAAGSGAGAGSGAGAGSGAGAGSGVGVPGVGV	622
Db	634	PGVGVPGKGVPGVGVPGVGVPGVGVPGAAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVGV	693
QY	623	GVGVGVGKGVPGVG- -GCVG- -PGVG- -PGVG- -PGAAGSGAGAGSGAGAGSGAGAGSGVGVPG	678
Db	694	GVGVGVGVPGKGVPGVGVPGVGVPGVGVPGAAGSGAGAGSGAGAGSGAGAGSGVGVPG	753
QY	679	VGVPGVGVPGKGVPGVG- -PGVG- -PGVG- -PGVG- -PGAAGSGAGAGSGAGAGSGAGAGSGV	734
Db	754	VGVPGVGVPGVGVPGKGVPGVGVPGVGVPGVGVPGAAGSGAGAGSGAGAGSGAGAGSGV	813
QY	735	GVPGVGVPGVGVPGKGVPGVG- -PGVG- -PGVG- -PGVG- -PGAAGSGAGAGSG	780
Db	814	GVPGGVGVPGVGVPGVGVPGKGVPGVGVPGVGVPGVGVPGAAGSGAGAGSG	863

CC	XX	AAVS1892
CC	XX	AAVS1882 standard; protein; 884 AA.
CC	XX	AAVS1882;
CC	XX	22-JUN-2000 (first entry)
CC	XX	Plasmid pET0345 protein fragment containing SELPK polymer units.
CC	XX	Crosslinked protein; fibrin glue; tissue adhesive; sealant; SELPK.
CC	XX	Synthetic.
CC	XX	US6033654-A.
CC	XX	07-MAR-2000.
CC	XX	02-MAY-1996; 96US-00642246.
CC	XX	05-MAY-1995; 95US-00435641.
CC	XX	(PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
CC	XX	Cappello J, Stedronsky ER;
CC	XX	WPI; 2000-255682/22.
CC	XX	Crosslinked protein composition, useful as tissue adhesive or sealant,
CC	XX	comprises peptide repeating units that contain functional groups reactive
CC	XX	with crosslinker.
CC	XX	Example 2; Col 51-56; 45pp; English.
CC	XX	This invention describes a novel crosslinked protein composition (A) in
CC	XX	which, before crosslinking, the protein (I) is new and comprises at least
CC	XX	70 wt.% of repeating units GAGGAS (1) and GGVGVP (2), and in at least two
CC	XX	repeating units an amino acid (aa) is substituted by Lys or Arg to
CC	XX	provide a Lys/Arg equivalent weight of 1-20 kD. (I) contains at least two

CC aa having a functional group reactive with at least one of aldehyde,
 CC iso(thio)cyanate and activated carboxy. (I) have similar biocompatibility
 CC to fibrin glue, but set more quickly and give a bond with greater shear
 CC strength. They are made from readily available natural sources, are easy
 CC to administer and are gradually resorbed. This sequence represents a
 CC crosslinking protein polymer unit designated SELP8K
 XX
 SQ Sequence 884 AA;

Query Match	82.6%	Score 3448;	DB 3;	Length 884;
Best Local Similarity	90.6%;	Pred. No. 6,-9e-217;		
Matches 752; Conservative	0;	Mismatches 26;	Indels 52;	Gaps 52;

[illegible]

RESULT 11
ABG31412
ID ABG31412 standard: protein: 884 AA.

XX	ABG31412;
AC	
XX	29-NOV-2002 (first entry)
DT	
XX	
DE	SELP8K polymer encoded by plasmid pPT0345.
XX	
XX	Protein polymer; functional group; crosslink; sealing; filling; tissue;
KW	tissue mass; tissue bonding; resorbable bond; flexible bond; sealant;
KW	adhesive; wound healing; burn dressing; blood flow; ruptured vessel;
KW	artery; vein; structural protein; vulnerrary; fibroin; elastin; collagen;
KW	keratin; SELP8K.
XX	
OS	Unidentified.
OS	Synthetic.
XX	
PN	US6423333-B1.
XX	
PD	23-JUL-2002.
XX	
PF	29-NOV-1999; 99US-00451206.
XX	
PR	05-MAY-1995; 95US-00435641.
XX	
PR	02-MAY-1996; 96US-00642246.
XX	
PA	(PROT-) PROTEIN POLYMER TECHNOLOGIES, INC.
XX	
PI	Stedronsky ER, Cappello J;
XX	
DR	WPI; 2002-672937/72.
XX	
PT	Crosslinked protein composition used as sealant or adhesive for sealing
PT	or filling defect in viable tissue, as burn dressing, or in wound healing
PT	e.g. to staunch flow of fluid e.g. blood, through ruptured vessels.
XX	
PS	Example 2; Col 17; 46pp; English.
XX	
XX	
CC	The present invention relates to protein polymers having repetitive units
CC	from naturally occurring structural proteins such as fibroin, elastin,
CC	collagen and keratin. The polymers comprise a functional group which can
CC	be chemically crosslinked with appropriate crosslinkers. The protein
CC	polymer is produced by recombinant DNA technology. The protein polymer is
CC	useful for sealing or filling a defect in viable tissue, particularly for
CC	augmenting tissue mass. The protein polymer is useful in a variety of
CC	applications related to their physical, chemical and biological
CC	properties, and/or to bond together separated tissue to provide a stable,
CC	flexible or resorbable bond. The protein is particularly useful as a
CC	sealant or adhesive, in wound healing or as a burn dressing e.g. to stop
CC	or staunch the flow of fluid (e.g. blood) through ruptured vessels (e.g.
CC	arteries or veins). The present sequence represents SELP8K polymer
XX	
XX	Sequence 884 AA;
XX	

Query Match	82.6%;	Score	3448;	DB 5;	Length	884;
Best Local Similarity	90.6%;	Pred.	No. 6.9e-217;			
Matches 752; Conservative	0;	Mismatches	26;	Indels	52;	Gaps 52;

QY	3	GAGSGAGAGSGSGVGPVGVPGVGPBKGVPGVC - PGVC - PGVC - PGVC - PGAGAGSGAGA	56
Db	34	GAGSGAGAGSGSGVGPVGVPGVGPBGKVPVGVPGVGPBGAGAGSGAGA	93
QY	59	GSAGAGSGAGAGSGSGVGPVGVPGVGPBGKVPGVG - PGVG - PGVG - PGVG - PGAGAGS	114
Db	94	GSAGAGSGAGAGSGSGVGPVGVPGVGPBGKVPBGVGPVGVGPBGVGPBGAGAGS	153
QY	115	GAGAGSGAGAGSGAGAGSGVGPVGVPGVGPBGKVPGVG - PGVG - PGVG - PGVG - PGA	170
Db	154	GAGAGSGAGAGSGAGAGSGVGPVGVPGVGPBGKVPBGVGPBGVGPBGVGPBGAG	213
QY	171	GAGSGAGAGSGAGAGAGSGAGAGSGVGPVGVPGVGPBGKVPBGV - PGVC - PGVC - PGVC - PGVC	227
Db	214	GAGSGAGAGSGAGAGSGAGAGSGVGPVGVPGVGPBGVGPBGKVPBGVGPBGVGPBGV	273

[illegible]

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RESULT 12
ABW01628
ID ABW01628 standard; protein; 884 AA.
XX
AC ABW01628;
XX
DT 12-FEB-2004 (first entry)
XX
DE Plaemid pPRO345 SELPAK polymer protein.
XX
XX Crosslinked protein; sealant; depot; drug; therapy; gel; film; thread;
KW coating; vulnery.
XX
OS Unidentified.
XX
PN US2003104589-A1.
XX
PD 05-JUN-2003.
XX
PF 05-APR-2002; 2002US-00117931.
XX
PR 05-MAY-1995; 95US-00435641.
XX
PR 02-MAY-1996; 96US-00642246.
XX
PR 29-NOV-1999; 99US-00451206.
XX
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
XX
PI Stedronsky ER, Cappello J;
XX
DR WPI; 2003-829350/77.
XX
PT Crosslinked protein composition useful as sealing a defect in tissue, the

```

PT protein prior to crosslinking comprises repetitive units of 3-15 amino acids of natural structural protein.

XX Example 2; Page 27-29; Opp; English.

XX The present invention relates to crosslinked protein composition. The invention is useful as sealants or depots to provide for relatively uniform release of a physiologically active product e.g., drug and for the formation of articles of manufacture such as gels, films, threads, coatings. The present sequence is plasmid pPT0345 SEU8K polymer protein CC
XX
XX Sequence 884 AA;

Query Match 82.6%; Score 3448; DB 7; Length 884;
Best Local Similarity 90.6%; Pred. No. 6.9e-217;
Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;

QY 3 GAGSGAGSGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGSGAGA 58
DB 34 GAGSGAGSGVPGVPGVPGVPGKGVPGVGPGVPGVPGAGSGAGA 93
QY 59 GSAGSGAGSGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGS 114
DB 94 GSAGSGAGSGVPGVPGVPGKGVPGVGPGVPGVPGAGAGS 153
QY 115 GAGAGSGAGSGAGSGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGA 170
DB 154 GAGAGSGAGSGAGSGVPGVPGVPGKGVPGVGPGVPGVPGAGAG 213
QY 171 GAGSGAGSGAGSGAGSGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG 227
DB 214 GAGSGAGSGAGSGAGSGVPGVPGVPGKGVPGVGPGVPGVPGVPGVG 273
QY 228 -PGAGSGAGSGAGSGAGSGAGSGVPGVPGVPGKGVPGVG-PGVG-PGVG- 283
DB 274 VPGAGAGSGAGSGAGSGAGSGAGSGVPGVPGVPGKGVPGVGPGVPGAGV 333
QY 284 PGVG-PGAGSGAGSGAGSGAGSGAGSGVPGVPGVPGKGVPGVG-PGVG-P 340
DB 334 PGVPGVPGAGSGAGSGAGSGAGSGAGSGVPGVPGVPGVPGVPGKGVPGV 393
QY 341 GVG-PGVG-PGAGSGAGSGAGSGAGSGAGSGVPGVPGVPGKGVPGVG-PG 397
DB 394 GVGPGVPGAGSGAGSGAGSGAGSGAGSGAGSGVPGVPGVPGVPGKGVPG 453
QY 398 VG-PGVG-PGVG-PGAGSGAGSGAGSGAGSGAGSGVPGVPGVPGKGVPGV 454
DB 454 VGPGVPGVPGVPGAGAGSGAGSGAGSGAGSGAGSGVPGVPGVPGVPGK 513
QY 455 G-PGVG-PGVG-PGAGSGAGSGAGSGAGSGAGSGAGSGVPGVPGVPGK 510
DB 514 GVPVPGVPGVPGVPGAGAGSGAGSGAGSGAGSGAGSGVPGVPGVPGV 573
QY 511 VPGVG-PGVG-PGVG-PGAGSGAGSGAGSGAGSGAGSGVPGVPGVPGV 566
DB 574 VPGAGVPGVPGVPGVPGAGAGSGAGSGAGSGAGSGAGSGVPGVPGV 633
QY 567 PGKGVPGVG-PGVG-PGVG-PGAGSGAGSGAGSGAGSGAGSGVPGVPGV 622
DB 634 PGVPGVPGVPGVPGVPGVPGAGAGSGAGSGAGSGAGSGAGSGVPGV 693
QY 623 GVGPGKGVPGVG-PGVG-PGVG-PGAGAGSGAGSGAGSGAGSGAGSGVPG 678
DB 694 GVGPGVPGKGVPGVPGVPGVPGAGAGSGAGSGAGSGAGSGAGSGVPG 753
QY 679 VGPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGSGAGSGAGSGV 734
DB 754 VGPGVPGVPGVPGKGVPGVPGVPGVPGAGAGSGAGSGAGSGAGSGAGV 813
QY 735 GVPVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGSGAGS 780
DB 814 GVPVPGVPGVPGVPGKGVPGVPGVPGVPGVPGAGAGSGAGSGAGS 863

RESULT 13
ID ADR70473 standard; protein; 884 AA.
XX
XX ADR70473;
AC
AC ADR70473;
DT 02-DEC-2004 (first entry)
XX
XX
DE Silk-elastin polymer SLP 47-E13.
XX
XX personal care composition; repeat sequence protein polymer;
KW hair care composition; shampoo; conditioner; anti-dandruff treatment;
KW styling aid; styling conditioner; hair repair treatment;
KW chemical hair treatment; hair dye; skin care composition; body wash;
KW antimicrobial cleanser; skin protectant cream; body lotion; facial cream;
KW moisturizing cream; facial cleanser; facial exfoliating gel;
KW surfactant-based facial cleanser; facial exfoliating gel;
KW anti-acne treatment; facial toner; exfoliating cream; facial mask;
KW after shave balm; sunscreen; anti-fungal treatment; skin protectant;
KW antiperspirant; cosmetic composition; makeup; eye gel;
KW high-melting point lipstick; lipstick; lip gloss; lip balm; mascara;
KW eyeliner; pressed powder formulation; foundation; nail care composition;
KW nail enamel; cuticle treatment; nail polish; nail treatment;
KW polish remover; oral care composition; toothpaste; mouth rinse;
KW breath freshener; teeth whitening treatment;
KW over-the-counter pharmaceutical composition; transparent film formation;
KW hydrogel formation; water-solubility; luster; softness;
KW glass retainer; tensile property; viscoelastic behaviour;
KW glass transition temperature; cloud temperature;
KW decomposition temperature; silk; elastin; repeating sequence unit.
XX
XX Synthetic.
OS
XX US2004180027-A1.
XX
XX 16-SEP-2004.
PD
XX 12-MAR-2004; 2004US-00800179.
XX
XX 12-MAR-2003; 2003US-0454077P.
PR
XX
XX (KUMAR/) KUMAR M.
PA (CUBV/) CUBVAS W A.
XX
XX Kumar M, Cuevas WA;
PI WPI; 2004-675584/66.
XX
XX Personal care composition useful as cosmetic, hair care or skin care
PT product, comprises repeat sequence protein polymer and compounds such as
PT carriers, excipients, liposomes, active ingredients, or emollients.
XX
XX Disclosure; SEQ ID NO 25; 50pp; English.
PS
XX The invention describes a personal care composition (I) comprising a
CC repeat sequence protein polymer with the balance of the composition
CC comprising one or more compounds chosen from carriers, excipients,
CC liposomes, active ingredients, biological or botanical products,
CC humectants, emollients, surfactants, thickening agents, silicone
CC components, organic sunscreens, preservatives, neutralizing agents,
CC perfumes and pigments. (I) is useful as a hair care composition such as
CC shampoo, conditioner, anti-dandruff treatment, styling aids, styling
CC conditioner, hair repair or treatment, serum, lotion, cream, pomade, or
CC chemical treatment such as hair dye; skin care composition such as
CC moisturizing body wash, body wash, antimicrobial cleanser, skin
CC protectant cream, body lotion, facial cream, moisturizing cream, facial
CC cleansing emulsion, surfactant-based facial cleanser, facial exfoliating
CC gel, anti-acne treatment, facial toner, exfoliating cream, facial mask,
CC after shave balm or sunscreen; skin care composition topically applied
CC over-the-counter drugs comprising anti-fungal treatments, anti-acne
CC treatments, skin protectants, and antiperspirants; cosmetic composition
CC comprising a makeup composition chosen from eye gel, high-melting point

CC lipstick, lipstick, lip gloss, lip balm, mascara, eyeliner, pressed
CC powder formulation and foundation; nail care composition such as nail
CC enamel, cuticle treatment, nail polish, nail treatment, or polish remover
CC ; an oral care composition such as toothpaste, mouth rinse, breath
CC freshener, or whitening treatment; and over-the-counter pharmaceutical
CC composition. The cosmetic composition is a mascara such as non-waterproof
CC mascara, waterproof mascara, volumizing mascara, lengthening mascara,
CC curling mascara, anhydrous waterproof mascara, water-based mascara, or
CC eyelash or eyebrow treatment; a pressed powder formulation such as loose
CC powder, blush, eye shadow, or bronzing powder; foundation such as water-
CC in-oil foundation, water-in-silicone foundation, oil-in-water foundation,
CC anhydrous makeup stick, or cream-to-powder foundation. (I) has desired
CC characteristics such as transparent film formation, hydrogel formation,
CC better efficacy and binding to skin, hair, nail, and oral surfaces,
CC desired level of hydrophobicity with water-solubility, imparting luster,
CC softness, moisture retentment, and mechanical properties (such as tensile
CC properties, viscoelastic behaviour, glass transition temperature, cloud
CC temperature and decomposition temperature), and does not have any
CC chemical modifications of the protein. This is the amino acid sequence of
CC silk-elastin polymer SLP 47-E13 that may be used as the repeat sequence
CC protein polymer of the invention.

XX
SQ Sequence 884 AA:

Query Match 82.6%; Score 3448; DB 8; Length 884;
Best Local Similarity 90.6%; Pred. No. 6,9e-217;
Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;

QY 3 GAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGAGAGSGAGA 58
DB 34 GAGSGAGAGSGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGV 93
QY 59 GSGAGAGSGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGS 114
DB 94 GSGAGAGSGAGSGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGV 153
QY 115 GAGAGSGAGAGSGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGA 170
DB 154 GAGAGSGAGAGSGAGSGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGV 213
QY 171 GAGSGAGAGSGAGSGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVG 227
DB 214 GAGSGAGAGSGAGSGAGSGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGV 273
QY 228 -PGAGSGAGAGSGAGSGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG- 283
DB 274 VPAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGVPGVGVPGVGVPGVGV 333
QY 284 PGVG-PGAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-P 340
DB 334 PGVGVPGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGVPGVGVPGVGVPGV 393
QY 341 GVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PG 397
DB 394 GVGPEPGVGVGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGVPGVGVPG 453
QY 398 VG-PGVG-PGAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG 454
DB 454 VGVPGVGPVGVPGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGVPGV 513
QY 455 G-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGVPGK 510
DB 514 GVGPGVGVPGVGPVGVPGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGV 573
QY 511 VPGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGV 566
DB 574 VPGVGVPGVGVPGVGPVGVPGAGAGSGAGAGSGAGAGSGVGVPGVGVPGV 633
QY 567 PGVGVPGVGV-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGVPGVGV 622
DB 634 PGVGVPGVGVPGVGPVGVPGVGVPGAGAGSGAGAGSGAGAGSGVGVPGV 693
QY 623 GVGVPGVGVPGVGV-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGVPG 678

DB 694 GVGVPVGVPGVGPVGVPGVGPVGVPGAGAGSGAGAGSGAGAGSGVGVPG 753
QY 679 VGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGV 734
DB 754 VGVPGVGPVGVPGVGPVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGV 813
QY 735 GVGVPVGVPGVGPVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGV 780
DB 814 GVGPGVPGVGVPGVGPVGVPGVGPVGVPGVGPVGVPGVGPVGVPGVGVPG 863

RESULT 14

ID ADU98735 standard; protein; 884 AA.

AC ADU98735;

DT 10-FEB-2005 (first entry)

DE Active agent release control system-related protein SeqID25.

KM cosmetics; delivery mechanism.

OS Unidentified.

PN US2004228913-A1.

PD 18-NOV-2004.

PF 14-MAY-2004; 2004US-00845775.

PR 14-MAY-2003; 2003US-0470465P.

PA (KUMA/) KUMAR M.

PA (MAZE/) MAZEAUD I.

PA (CHRI/) CHRISTIANO S P.

PI Kumar M, Mazeaud I, Christiano SP;

DR WPI; 2005-037015/04.

PT System for providing controlled release delivery of active agent useful
PT for incorporating active agents into personal care product compositions,
PT comprises repeat sequence protein polymer and active agent.

PS Disclosure; SEQ ID NO 25; 34pp; English.

XX This invention relates to a novel system for providing controlled release
XX delivery of an active agent which comprises a repeat sequence protein
XX polymer and at least one active agent. The invention may be useful in a
XX hair care composition, skin care composition, nail care composition,
XX cosmetic composition, oral care composition or over-the-counter
XX pharmaceutical composition. The system may be useful in shampoo, gels,
XX mousses and other hair care products, rinse-off conditioners, skin care
XX products such as moisturizers, toners and makeup and nail care products
XX such as polishes and polish removers. The invention enables controlled
XX release of active agents. The present sequence is that of a protein which
XX is related to the invention.

SQ Sequence 884 AA:

Query Match 82.6%; Score 3448; DB 9; Length 884;
Best Local Similarity 90.6%; Pred. No. 6,9e-217;
Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;

QY 3 GAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGAGAGSGAGA 58
DB 34 GAGSGAGAGSGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGV 93
QY 59 GSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGS 114
DB 94 GSGAGAGSGAGAGSGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGV 153

Db 214 GAGSGAGAGSGAGAGSGAGGCGVGPVGVPGVGPBGEGVPGVGPBGVGPBGVGPBGVGP 273
QY 228 - PGAGAGSGAGAGSGAGAGSGAGGCGVGPVGVPBGVGPBGVGPBGVGPBGVGPBGVGP 283
Db 274 VPAGAGSGAGAGSGAGAGSGAGGCGVGPVGVPBGVGPBGVGPBGVGPBGVGPBGVGP 333
QY 284 PGVGP-PGAGAGSGAGAGSGAGAGSGAGGCGVGPVGVPBGVGPBGVGPBGVGPBGVGP-P 340
Db 334 PGVGP-PGAGAGSGAGAGSGAGAGSGAGGCGVGPVGVPBGVGPBGVGPBGVGPBGVGP 393
QY 341 GVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGGCGVGPVGVPBGVGPBGVGPBGVGP-PG 397
Db 394 GVGEPGVGPAGAGSGAGAGSGAGGCGVGPVGVPBGVGPBGVGPBGVGPBGVGPBGVGP 453
QY 398 VG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGGCGVGPVGVPBGVGPBGVGPBGVGP 454
Db 454 VGVPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGP 513
QY 455 G-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGGCGVGPVGVPBGVGPBGVGPBGVGP 510
Db 514 GVPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGP 573
QY 511 VPGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGGCGVGPVGVPBGVGPBGVGP 566
Db 574 VPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGP 633
QY 567 PGKGVPGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGGCGVGPVGVPBGVGP 622
Db 634 PGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGP 693
QY 623 GVGVPBGVGPBGVGP-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGGCGVGPVG 678
Db 694 GVGVPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGP 753
QY 679 VGVPBGVGPBGVGPBGVGP-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGGCGV 734
Db 754 VGVPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGP 813
QY 735 GVPBGVGPBGVGPBGVGPBGVGP-PGVG-PGVG-PGAGAGSGAGAGSGAGGCGV 780
Db 814 GVPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGPBGVGP 863

Search completed: May 10, 2006, 10:39:41
Job time : 195 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 10, 2006, 10:43:59 ; Search time 47 Seconds
(without alignments)
1372.064 Million cell updates/sec

Title: US-10-800-179-19

Perfect score: 4173
Sequence: 1 GAAGSGAGAGSGGVPGVC.....GVPGVPGAGAGSGAGAGS 780

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

- Database : Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
 - 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
 - 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
 - 4: /cgn2_6/ptodata/1/iaa/PCRTUS_COMB.pep:*
 - 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
 - 6: /cgn2_6/ptodata/1/iaa/backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3526	84.5	889	2 US-08-806-029-19	Sequence 19, Appl
2	3448	82.6	884	1 US-08-397-633A-68	Sequence 68, Appl
3	3448	82.6	884	1 US-08-435-641-15	Sequence 15, Appl
4	3448	82.6	884	1 US-08-707-237A-96	Sequence 96, Appl
5	3448	82.6	884	2 US-08-642-246-15	Sequence 15, Appl
6	3448	82.6	884	2 US-09-451-206-15	Sequence 15, Appl
7	3448	82.6	884	4 PCT-US96-06229-15	Sequence 15, Appl
8	3296	79.0	2257	1 US-08-175-155-47	Sequence 47, Appl
9	3296	79.0	2257	1 US-08-477-509B-82	Sequence 82, Appl
10	3296	79.0	2257	1 US-08-707-237A-53	Sequence 82, Appl
11	3296	79.0	2257	2 US-08-482-085B-82	Sequence 82, Appl
12	3296	79.0	2257	2 US-09-444-791A-82	Sequence 82, Appl
13	3284	78.7	877	1 US-08-397-633A-54	Sequence 54, Appl
14	3253	78.0	832	1 US-08-212-237-4	Sequence 4, Appl
15	3253	78.0	832	2 US-08-806-029-27	Sequence 27, Appl
16	3253	78.0	832	4 PCT-US95-02772-4	Sequence 4, Appl
17	3192	76.5	768	2 US-08-806-029-35	Sequence 35, Appl
18	3182	76.3	988	1 US-08-212-237-5	Sequence 5, Appl
19	3182	76.3	988	2 US-08-806-029-28	Sequence 28, Appl
20	3182	76.3	988	4 PCT-US95-02772-5	Sequence 5, Appl
21	3176	76.1	1413	1 US-08-175-155-39	Sequence 39, Appl
22	3176	76.1	1413	1 US-08-707-237A-45	Sequence 45, Appl
23	3176	76.1	1464	1 US-08-477-509B-74	Sequence 74, Appl
24	3176	76.1	1464	2 US-08-482-085B-74	Sequence 74, Appl
25	3158	75.7	2055	1 US-09-444-791A-74	Sequence 74, Appl
26	3158	75.7	2055	1 US-08-175-155-46	Sequence 46, Appl
27	3158	75.7	2055	1 US-08-477-509B-81	Sequence 81, Appl

28	3158	75.7	2055	1 US-08-707-237A-52	Sequence 52, Appl
29	3158	75.7	2055	2 US-08-482-085B-81	Sequence 81, Appl
30	3158	75.7	2055	2 US-09-444-791A-81	Sequence 81, Appl
31	3089	74.0	2018	2 US-09-444-791A-80	Sequence 80, Appl
32	3089	74.0	2100	1 US-08-477-509B-80	Sequence 80, Appl
33	3089	74.0	2100	2 US-08-482-085B-80	Sequence 80, Appl
34	3089	74.0	2107	1 US-08-175-155-45	Sequence 45, Appl
35	3089	74.0	2107	1 US-08-707-237A-51	Sequence 51, Appl
36	2998	71.8	1056	1 US-08-212-237-6	Sequence 6, Appl
37	2998	71.8	1056	2 US-08-806-029-29	Sequence 29, Appl
38	2998	71.8	1056	4 PCT-US95-02772-6	Sequence 6, Appl
39	2855	68.4	1002	1 US-08-707-237A-103	Sequence 103, App
40	2855	68.4	1002	2 US-08-642-246-25	Sequence 25, Appl
41	2855	68.4	1002	2 US-09-451-206-25	Sequence 25, Appl
42	2855	68.4	1002	4 PCT-US96-06229-25	Sequence 25, Appl
43	2830	67.8	750	2 US-08-806-029-25	Sequence 25, Appl
44	2814	67.4	696	2 US-08-806-029-36	Sequence 36, Appl
45	2795	67.0	936	1 US-08-707-237A-106	Sequence 106, App

ALIGNMENTS

RESULT 1
US-08-806-029-19
Sequence 19, Application US/08806029
Patent No. 6380154
GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
APPLICANT: Stedronsky, Erwin R.
TITLE OF INVENTION: Synthetic Proteins for in vivo Drug
TITLE OF INVENTION: Delivery and Tissue Augmentation
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Teet, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/806,029
FILING DATE: 24-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,237
FILING DATE: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58847-2/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 889 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-806-029-19
Query Match 84.5%; Score 3526; DB 2; Length 889;
Best Local Similarity 92.2%; Pred. No. 5.6e-254;
Matches 765; Conservative 0; Mismatches 13; Indels 52; Gaps 52;
QY 3 GAAGSGAGAGSGGVPGVPGVPGAGAGSGAGAGS 58

[illegible]

RESULT 2
 US-08-397-633A-C6
 ; Sequence 68, Application US/08397633A
 ; Patent No. 5773577
 ; GENERAL INFORMATION:
 ; APPLICANT: Cappello, Joseph
 ; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
 ; TITLE OF INVENTION: OF ENZYMAITC CROSS-LINKING
 ; NUMBER OF SEQUENCES: 105
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FLIER, HOBACH, TEST, ALBRITTON & HERBERT
 ; STREET: 4 Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-4187
 ;
 ; COMPUTER READABLE FORM:

```

1 MEDIUM TYPE: Floppy disk
2 COMPUTER: IBM PC compatible
3 OPERATING SYSTEM: PC-DOS/MS-DOS
4 SOFTWARE: Patent In Release #1.0, Version #1.25
5 CURRENT APPLICATION DATA:
6 APPLICATION NUMBER: US/08/397,633A
7 FILING DATE:
8
9 CLASSIFICATION: 530
10 ATTORNEY/AGENT INFORMATION:
11 NAME: Rowland, Bertram I
12 REGISTRATION NUMBER: 20,015
13 REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: (415) 781-1989
16 TELEFAX: (415) 398-3249
17 TELEX: 910 277299
18 INFORMATION FOR SEQ ID NO: 68:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 884 amino acids
21 TYPE: amino acid
22 STRANDEDNESS: single
23 TOPOLOGY: linear
24 MOLECULE TYPE: protein
25
26 US-08-397-633A-68

```

Query Match	82.6%	Score 3448	DB 1	Length 884	
Best Local Similarity	90.6%	Pred. No. 3.3e-249			
Matches 752	Conservative 0	Mismatches 26	Indels 52	Gaps 52	
QY	3	GAGSGAGAGSGVGPVGVPPGVGPVGKGPVG- -PGVG- -PGVG- -PGVG- -PGAAGAGSAGA	58		
DB	34	GAGSGAGAGSGVGPVGVPPGVGPVGKGPVGVPVGVGPVGAAGAGSAGA	93		
QY	59	GSAGAGSGAGAGSGVGPVGVPPGVGPVGKGPVG- -PGVG- -PGVG- -PGAAGS	114		
DB	94	GSAGAGSGAGAGSGVGPVGVPPGVGPVGKGPVGVPVGVGPVGAAGS	153		
QY	115	GAGAGSGAGAGSGAGAGSGVPPGVGPVGVPKGPVG- -PGVG- -PGVG- -PGA	170		
DB	154	GAGAGSGAGAGSGAGAGSGVPPGVGPVGVPKGPVGVPVGVGPVGA	213		
QY	171	GAGSGAGAGSGAGAGSGVGPVGPVGPVGPVGKGPVG- -PGVG- -PGVG- -PGVG	227		
DB	214	GAGSGAGAGSGAGAGSGVGPVGPVGPVGPVGKGPVGVPVGPVGPVGVPVG	273		
QY	228	-PGAAGSGAGAGSGAGAGSGVGPVGPVGPVGKGPVG- -PGVG- -PGVG-	283		
DB	274	VPGAAGSGAGAGSGAGAGSGVGPVGPVGPVGPVGKGPVGVPVGPVG	333		
QY	284	PGVG- -PGAAGSGAGAGSGAGAGSGVGPVGPVGPVGPVGKGPVG- -PGVG- -P	340		
DB	334	PGVVPGAAGSGAGAGSGAGAGSGVGPVGPVGPVGPVGPVGKGPVGVP	393		
QY	341	GVG- -PGVG- -PGAAGSGAGAGSGAGAGSGVGPVGPVGPVGPVGKGPVG- -PG	397		
DB	394	GVGPVGPVPGAAGSGAGAGSGAGAGSGVGPVGPVGPVGPVGKGPVG	453		
QY	398	VG- -PGVG- -PGAAGSGAGAGSGAGAGSGVGPVGPVGPVGPVGKGPVG	454		
DB	454	VGVGPVGPVGPVPGAAGSGAGAGSGAGAGSGVGPVGPVGPVGPVGKGPVG	513		
QY	455	G- -PGVG- -PGVG- -PGAAGSGAGAGSGAGAGSGVGPVGPVGPVGPVGKGPVG	510		
DB	514	GVGPVGPVGPVGPVPGAAGSGAGAGSGAGAGSGVGPVGPVGPVGPVGKGPVG	573		
QY	511	VPVG- -PGVG- -PGVG- -PGAAGSGAGAGSGAGAGSGVGPVGPVGPVG	566		
DB	574	VPKGPVGPVGPVGPVPGAAGSGAGAGSGAGAGSGVGPVGPVGPVG	633		
QY	567	PGKVPVGPV- -PGVG- -PGVG- -PGAAGSGAGAGSGAGAGSGVGPVGPVG	622		
DB	634	PGVVPVGPVGPVGPVPGAAGSGAGAGSGAGAGSGVGPVGPVG	693		

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/609,716
FILING DATE: 06-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/269,429
FILING DATE: 09-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-10/MHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 884 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-707-237A-96

Query Match 82.6%; Score 3448; DB 1; Length 884;

Best Local Similarity 90.6%; Pred. No. 3.3e-248; Indels 52; Gaps 52;
Matches 752; Conservative 0; Mismatches 26;

QY 3 GAGSGAGAGSGVGPVGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSGAGA 58
DB 34 GAGSGAGAGSGVGPVGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSGAGA 93
QY 59 GAGGAGAGAGSGVGPVGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGS 114
DB 94 GAGGAGAGAGSGVGPVGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGS 153
QY 115 GAGAGSGAGAGSGAGSGVGPVGVPGVPGKGVPGVG-PGVG-PGVG-PGA 170
DB 154 GAGAGSGAGAGSGAGSGVGPVGVPGVPGKGVPGVG-PGVG-PGVG-PGA 213
QY 171 GAGSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGVG-PGVG-PGVG-PGVG 227
DB 214 GAGSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGVG-PGVG-PGVG-PGVG 273
QY 228 -PGAGAGSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGVG-PGVG-PGVG- 283
DB 274 VPAGAGAGSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGVG-PGVG-PGVG- 333
QY 284 PGVG-PGAGAGSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGVG-PGVG-P 340
DB 334 PGVG-PGAGAGSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGVG-PGVG-P 393
QY 341 GVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGVG-PG 397
DB 394 GVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGVG-PG 453
QY 398 VG-PGVG-PGAGAGSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGV 454
DB 454 VGVPGVPGVGPVPGAGAGSGAGAGSGAGAGSGVGPVGVPGVPGKGVPG 513
QY 455 G-PGVG-PGVG-PGVG-PGAAGSGAGAGSGAGAGSGVGPVGVPGVPGK 510
DB 514 GVPGVGPVGPVGPVPGAGAGSGAGAGSGAGAGSGVGPVGVPGVPGVPG 573
QY 511 VPGVG-PGVG-PGVG-PGVG-PGAAGSGAGAGSGAGAGSGVGPVGVPGV 566

DB 574 VPGKGVPGVGPVGPVPGAGAGSGAGAGSGAGAGSGVGPVGPVGPV 633
QY 567 PGKGVPGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGPVGPV 622
DB 634 PGVGPVPGVGPVGPVGPVPGAGAGSGAGAGSGAGAGSGVGPVGPV 693
QY 623 GVPVPGKGVPGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGPV 678
DB 694 GVPVGPVPGKGVPGVGPVGPVPGAGAGSGAGAGSGAGAGSGVGPV 753
QY 679 VGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGV 734
DB 754 VGVPGVGPVGPVPGKGVPGVGPVGPVPGAGAGSGAGAGSGAGAGSGV 813
QY 735 GVPVGPVPGVGPVPGKGVPGVG-PGVG-PGVG-PGAGAGSGAGAGS 780
DB 814 GVPVGPVPGVGPVPGKGVPGVGPVGPVPGAGAGSGAGAGS 863

RESULT 5

US-08-642-246-15
Sequence 15, Application US/08642246
Patent No. 6033654
GENERAL INFORMATION:
APPLICANT: STEDRONSKY, Erwin R.
TITLE OF INVENTION: Tissue Adhesive Using Synthetic
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSER: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: Four Embarcadero Center, Suite 200
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,246
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Berttram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A61127-1/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 884 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-642-246-15

Query Match 82.6%; Score 3448; DB 2; Length 884;

Best Local Similarity 90.6%; Pred. No. 3.3e-248; Indels 52; Gaps 52;
Matches 752; Conservative 0; Mismatches 26;

QY 3 GAGSGAGAGSGVGPVGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSGAGA 58
DB 34 GAGSGAGAGSGVGPVGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSGAGA 93
QY 59 GSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGS 114
DB 94 GSGAGAGSGAGAGSGVGPVGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGS 153

[illegible]

```

PCT-US96-06229-15          : Sequence 15, Application PC/TUS9606229
GENERAL INFORMATION:
APPLICANT: STEDRONSKY, Erwin R.
APPlicant: CAPPELLO, Joseph
TITLE OF INVENTION: Tissue Adhesive Using Synthetic
TITLE OF INVENTION: Crosslinking
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: Four Embarcadero Center, Suite 200
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06229
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I
REGISTRATION NUMBER: 20015
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: A61127-1/BIR
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ. ID NO.: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 884 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-06229-15

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Query Match	82.6%;	Score	3448;	DB	4;	Length	884;
Best Local Similarity	90.6%;	Pred.	No. 3.3e-248;				
Matches	752;	Conservative	0;	Mismatches	26;	Indels	52;
						Gaps	52;

[illegible][illegible]

RESULT 8
 US-08-175-155-47
 Sequence 47, Application US/08175155
 Patent No. 5641648
 GENERAL INFORMATION:
 APPLICANT: Ferrari, Franco A.
 APPLICANT: Cappello, Joseph
 APPLICANT: Cristman, John W.
 APPLICANT: Dorman, Mary A.
 TITLE OF INVENTION: Methods for Preparing Synthetic
 TITLE OF INVENTION: Repetitive DNA
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fleht, Hobdach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: CA
 COUNTRY: US
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/175,155
 FILING DATE: 29-DEC-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Rowland, Bertram I.
 REGISTRATION NUMBER: 20015
 REFERENCE/DOCKET NUMBER: A-55186-5/BIR
 TELECOMMUNICATION INFORMATION:

ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I.
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-55186-5/BIR
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2257 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-175-155-47

Query Match 79.0%; Score 3296; DB 1; Length 2257;
Best Local Similarity 67.4%; Pred. No. 1.3e-236;
Matches 755; Conservative 0; Mismatches 25; Indels 340; Gaps 52;

QY 1 GAGAGSAGAGSGVPGVPGVPGVPGKGVPGV-G-PGVG-PGVG-PGV----- 46
DB 38 GAGAGSAGAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 97
QY 47 -----GPGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 92
DB 98 GAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 157
QY 93 GVG-PGVG-PGV-----GPGAGSGAGAGSGAGA 124
DB 158 GVGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 217
QY 125 GSGAGAGSGVPGVPGVPGVPGKGVPGV-G-PGVG-PGVG-PGV----- 166
DB 218 GSGAGAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 277
QY 167 -----GPGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 215
DB 278 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 337
QY 216 PGVG-PGVG-PGV-----GPGAGSGAGAGSGAGAGSGA 248
DB 338 PGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 397
QY 249 GAGSGVPGVPGVPGVPGKGVPGV-G-PGVG-PGVG-PGV----- 286
DB 398 GAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 457
QY 287 -----GPGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 339
DB 458 GSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 517
QY 340 -PGVG-PGV-----GPGAGSGAGAGSGAGAGSGAGA 372
DB 518 VPVGVPVGVPVPGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGA 577
QY 373 GVGVPVGVPVPGVPGKGVPGV-G-PGVG-PGVG-PGV----- 406
DB 578 GVGVPVGVPVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 637
QY 407 --GPGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 462
DB 638 GAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 697
QY 463 G-PGV-----GPGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 496
DB 698 GVPVGVPVPGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 757
QY 497 PGVVPVGVPVPGKGVPGV-G-PVG-PGVG-PGV-----GP 528
DB 758 PGVVPVGVPVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 817
QY 529 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 585
DB 818 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 877
QY 586 V-----GPGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 620

DB 878 VGPVPGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 937
QY 621 VPVGVPVPGKGVPGV-G-PVG-PGVG-PGV-----GPGAGA 652
DB 938 VPVGVPVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 997
QY 653 GSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 706
DB 998 GSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 1057
QY 707 -----GPGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 744
DB 1058 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 1117
QY 745 GVPKGVPGV-G-PVG-PGVG-PGV-G-PAGAGSGAGAGSG 780
DB 1118 GVPVGVPVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 1157

RESULT 9
US-08-477-509B-82
Sequence 82, Application US/08477509B
Patent No. 5770697
GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A
APPLICANT: Cappello, Joseph
APPLICANT: Crissman, John W
APPLICANT: Dorman, Mary A
TITLE OF INVENTION: No. 5770697e1 Peptides Comprising Repetitive
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,509B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 2257 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

[illegible]

[illegible][illegible]

[illegible]

RESULT 13
US-08-397-633A-54
; Sequence 54, Application US/08397633A
; Patent No. 5773577

```

1 GENERAL INFORMATION:
2 APPLICANT: Cappello, Joseph
3 TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
4 TITLE OF INVENTION: OF ENZYMTATIC CROSS-LINKING
5 NUMBER OF SEQUENCES: 105
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
8 STREET: 4 Embarcadero Center, Suite 3400
9 CITY: San Francisco
10 STATE: California
11 COUNTRY: USA
12 ZIP: 94111-4187
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: Patent'n Release #1.0, Version #1.25
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/397,633A
20 FILING DATE:
21 CLASSIFICATION: 530
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Rowland, Bertram I
24 REGISTRATION NUMBER: 20,015
25 REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: (415) 781-1989
28 TELEFAX: (415) 398-3249
29 TELEX: 910 277299
30 INFORMATION FOR SEQ ID NO: 54:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 877 amino acids
33 TYPE: amino acid
34 STRANDEDNESS: single
35 TOPOLOGY: linear
36 MOLECULE TYPE: protein
37
38 US-08-397-633A-54

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Query Match	Similarity	Score	DB 1:	Length
Best Local Match	78.7%;	89.9%;	Pred. No. 4.5e-236;	877;
Matches	718;	Conservative	1;	Mismatches 22; Indels 58; Gaps 50.
QY	3	GAGSGAGAGSGGCGVPGVGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGA GSGAGA	58	
Db	57	GAGSGAGAGSGGCGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGAGA GSGAGA	116	
QY	59	GSGAGAGSGAGAGSGGCGVPGVGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGA GGS	114	
Db	117	GSGAGAGSGAGAGSGGCGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGAGA GGS	176	
QY	115	GAGAGSGAGAGSGAGAGSGGCGVPGVGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGA	170	
Db	177	GAGAGSGAGAGSGAGAGSGGCGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGAGA	236	
QY	171	GAGSGAGAGSGAGAGSGGCGVPGVGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGVG	227	
Db	237	GAGSGAGAGSGAGAGSGGCGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVG	296	
QY	228	- PGAGAGSGAGAGSGAGAGSGGCGVPGVGVPGVGVPGKGVPGVG - PGVG - PGVG -	283	
Db	297	VPGAGAGSGAGAGSGAGAGSGGCGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVG	356	
QY	284	PGVG - PGAGAGSGAGAGSGAGAGSGGCGVPGVGVPGVGVPGKGVPGVG - PGVG - P	340	
Db	357	PGVGVPGAGAGSGAGAGSGAGAGSGGCGVPGVGVPGVGVPGVGVPGVGVPGVGVPG	416	
QY	341	GVG - PGVG - PGAGAGSGAGAGSGAGAGSGGCGVPGVGVPGVGVPGKGVPGVG - PG	397	
Db	417	GVGVPGVGVPGAGAGSGAGAGSGAGAGSGGCGVPGVGVPGVGVPGVGVPGVGVPGVG	476	
QY	398	VG - PGVG - PGVG - PGAGAGSGAGAGSGAGAGSGGCGVPGVGVPGVGVPGKGVPGV	454	
Db	477	VGVGVGVPGVGVPGAGAGSGAGAGSGAGAGSGGCGVPGVGVPGVGVPGVGVPGVGVPGV	536	

QY	455	G-PGVG--PGVG--PGVG--PGAAGSGSAGAGSGSAGAGSGSAGAGSGVGPVGVPVGVP	PGKG	510
Db	537	GVPGVGVGVGVPGVGPBAGAGSGAGAGSGAGAGSGAGAGSGVGPVGVPVGVP	PGVG	596
QY	511	VPGVG--PGVG--PGVG--PGVG--PGAAGSGSAGAGSGSAGAGSGVGPVGVPVGVP		566
Db	597	VPGVGVPGVGVPGVGPVPGVGPBAGAGSGAGAGSGAGAGSGVGPVGVPVGVP		656
QY	567	PGKGVPGVG--PGVG--PGVG--PGVG--PGAAGSGSAGAGSGSAGAGSGVGPVGVP		622
Db	657	PGVGPVGVPVGVPVGVPVGVPBAGAGSGAGAGSGSAGAGSGVGPVGVP		716
QY	623	GVGVPGKGVPGVG--PGVG--PGVG--PGVG--PGAAGSGSAGAGSGSAGAGSGVGPVG		678
Db	717	GVGVPGVGVPGVGPVGVPVGVPBAGAGSGAGAGSGSAGAGSGVGPVG		776
QY	679	VGVGPGVGPVGKGVPGVG--PGVG--PGVG--PGVG--PGAAGSGSAGAGSGA	-----GSAAGG	731
Db	777	VGVPVGVPBAGVPGVGPVGVPVGVPBAGAGSGAGAGSGA	GAMPDGRYHMA	836
QY	732	SGVGPVGVPVGVPVGVP	750	
Db	837	KGDRAPE-----GTPGEG	948	

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RESULT 14
US-08-212-237-4
; Sequence 4, Application US/08212237
; Patent No. 5606019
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: Synthetic Proteins As Implantables
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Honbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212, 237
; FILING DATE: 11-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58847/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 832 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-212-237-4

```

	Query Match	78.0%	Score 3253;	DB 1:	Length 832;
	Best Local Similarity	88.9%	Pred. No. 8.5e-234;		
	Matches 742; Conservative	0;	Mismatches 11;	Indels 80;	Gaps 65;
Oy	9 GAGSGVGVGVGVPGVGVPKGVPGVG-PGVG-PGVGPFGAGSAGAGSGAGAG	65			
Db	3 G-----VGVPKGVPGVGVGVGVGVPGVGVPKGVPGVG-PGVGPFGAGSAGAGSGAAG	57			

[illegible]

```

/ RESULT 15
/ US-08-806-029-27
/ Sequence 27, Application US/08806029
/ Patent No. 6380154
/
/ GENERAL INFORMATION:
/
/ APPLICANT: Cappello, Joseph
/ APPLICANT: Stedronsky, Erwin R.
/ TITLE OF INVENTION: Synthetic Proteins for in vivo Drug
/ TITLE OF INVENTION: Delivery and Tissue Augmentation
/
/ NUMBER OF SEQUENCES: 36
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSSEE: Flehr, Hochbach, Test, Albritton & Herbert
/ STREET: Four Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States
/ ZIP: 94111
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/

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Db	301	GAGAGSGAGAGSGVGP	PGVGVP	PGVGVP	PGKGV	PGVGP	PGVGP	PGVGP	PGVGP	PGAGAGSGAGAGS	360
Qy	361	GAGAGSGAGAGSGVGP	PGVGVP	PGVGVP	PGKGV	PGVGP	PGVGP	PGVGP	PGVGP	PGAGAGSGAGAGS	420
Db	361	GAGAGSGAGAGSGVGP	PGVGVP	PGVGVP	PGKGV	PGVGP	PGVGP	PGVGP	PGVGP	PGAGAGSGAGAGS	420
Qy	421	GAGAGSGAGAGSGVGP	PGVGVP	PGVGVP	PGKGV	PGVGP	PGVGP	PGVGP	PGVGP	PGAGAGSGAGAGS	480
Db	421	GAGAGSGAGAGSGVGP	PGVGVP	PGVGVP	PGKGV	PGVGP	PGVGP	PGVGP	PGVGP	PGAGAGSGAGAGS	480
Qy	481	GAGAGSGAGAGSGVGP	PGVGVP	PGVGVP	PGKGV	PGVGP	PGVGP	PGVGP	PGVGP	PGAGAGSGAGAGS	540
Db	481	GAGAGSGAGAGSGVGP	PGVGVP	PGVGVP	PGKGV	PGVGP	PGVGP	PGVGP	PGVGP	PGAGAGSGAGAGS	540
Qy	541	GAGAGSGAGAGSGVGP	PGVGVP	PGVGVP	PGKGV	PGVGP	PGVGP	PGVGP	PGVGP	PGAGAGSGAGAGS	600
Db	541	GAGAGSGAGAGSGVGP	PGVGVP	PGVGVP	PGKGV	PGVGP	PGVGP	PGVGP	PGVGP	PGAGAGSGAGAGS	600
Qy	601	GAGAGSGAGAGSGVGP	PGVGVP	PGVGVP	PGKGV	PGVGP	PGVGP	PGVGP	PGVGP	PGAGAGSGAGAGS	660
Db	601	GAGAGSGAGAGSGVGP	PGVGVP	PGVGVP	PGKGV	PGVGP	PGVGP	PGVGP	PGVGP	PGAGAGSGAGAGS	660
Qy	661	GAGAGSGAGAGSGVGP	PGVGVP	PGVGVP	PGKGV	PGVGP	PGVGP	PGVGP	PGVGP	PGAGAGSGAGAGS	720
Db	661	GAGAGSGAGAGSGVGP	PGVGVP	PGVGVP	PGKGV	PGVGP	PGVGP	PGVGP	PGVGP	PGAGAGSGAGAGS	720
Qy	721	GAGAGSGAGAGSGVGP	PGVGVP	PGVGVP	PGKGV	PGVGP	PGVGP	PGVGP	PGVGP	PGAGAGSGAGAGS	780
Db	721	GAGAGSGAGAGSGVGP	PGVGVP	PGVGVP	PGKGV	PGVGP	PGVGP	PGVGP	PGVGP	PGAGAGSGAGAGS	780

[illegible]

Dd	181	GAGAGSGAGAGSGVGPBGVGPBGVGPBGKVPBGVGPBGVGPBGVGPBGVGPBGAGAGSGAGAGS	240
Qy	241	GAGAGSGAGAGSGVGPBGVGPBGVGPBGKVPBGVGPBGVGPBGVGPBGVGPBGAGAGSGAGAGS	300
Dd	241	GAGAGSGAGAGSGVGPBGVGPBGVGPBGKVPBGVGPBGVGPBGVGPBGVGPBGAGAGSGAGAGS	300
Qy	301	GAGAGSGAGAGSGVGPBGVGPBGVGPBGKVPBGVGPBGVGPBGVGPBGVGPBGAGAGSGAGAGS	360
Dd	301	GAGAGSGAGAGSGVGPBGVGPBGVGPBGKVPBGVGPBGVGPBGVGPBGVGPBGAGAGSGAGAGS	360
Qy	361	GAGAGSGAGAGSGVGPBGVGPBGVGPBGKVPBGVGPBGVGPBGVGPBGVGPBGAGAGSGAGAGS	420
Dd	361	GAGAGSGAGAGSGVGPBGVGPBGVGPBGKVPBGVGPBGVGPBGVGPBGVGPBGAGAGSGAGAGS	420
Qy	421	GAGAGSGAGAGSGVGPBGVGPBGVGPBGKVPBGVGPBGVGPBGVGPBGVGPBGAGAGSGAGAGS	480
Dd	421	GAGAGSGAGAGSGVGPBGVGPBGVGPBGKVPBGVGPBGVGPBGVGPBGVGPBGAGAGSGAGAGS	480
Qy	481	GAGAGSGAGAGSGVGPBGVGPBGVGPBGKVPBGVGPBGVGPBGVGPBGVGPBGAGAGSGAGAGS	540
Dd	481	GAGAGSGAGAGSGVGPBGVGPBGVGPBGKVPBGVGPBGVGPBGVGPBGVGPBGAGAGSGAGAGS	540
Qy	541	GAGAGSGAGAGSGVGPBGVGPBGVGPBGKVPBGVGPBGVGPBGVGPBGVGPBGAGAGSGAGAGS	600
Dd	541	GAGAGSGAGAGSGVGPBGVGPBGVGPBGKVPBGVGPBGVGPBGVGPBGVGPBGAGAGSGAGAGS	600
Qy	601	GAGAGSGAGAGSGVGPBGVGPBGVGPBGKVPBGVGPBGVGPBGVGPBGVGPBGAGAGSGAGAGS	660
Dd	601	GAGAGSGAGAGSGVGPBGVGPBGVGPBGKVPBGVGPBGVGPBGVGPBGVGPBGAGAGSGAGAGS	660
Qy	661	GAGAGSGAGAGSGVGPBGVGPBGVGPBGKVPBGVGPBGVGPBGVGPBGVGPBGAGAGSGAGAGS	720
Dd	661	GAGAGSGAGAGSGVGPBGVGPBGVGPBGKVPBGVGPBGVGPBGVGPBGVGPBGAGAGSGAGAGS	720
Qy	721	GAGAGSGAGAGSGVGPBGVGPBGVGPBGKVPBGVGPBGVGPBGVGPBGVGPBGAGAGSGAGAGS	780
Dd	721	GAGAGSGAGAGSGVGPBGVGPBGVGPBGKVPBGVGPBGVGPBGVGPBGVGPBGAGAGSGAGAGS	780

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RESULT 3
US-10-845-775A-19
; Sequence 19, Application US/10845775A
; Publication No. US20040228913A1
; GENERAL INFORMATION:
; APPLICANT: Kumar, Manoj
; APPLICANT: Mazaud, Isabelle
; APPLICANT: Christiano, Steven P.
; TITLE OF INVENTION: Controlled Release of Active Agents Utilizing Repeat Sequence
; TITLE OF INVENTION: Protein Polymers
; FILE REFERENCE: DOC 0077 PA/GC 792-6/DC 5110
; CURRENT APPLICATION NUMBER: US/10/845,775A
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/470,465
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 780
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: silk and elastin peptide repeats
US-10-845-775A-19

Query Match      100.0%; Score 4173; DB 5; Length 780;
Best Local Similarity 100.0%; Pred. No. 6,66-248;
Matches 780; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGAGSGAGAGSGVGPVGVPGVGPGKGVPGVGPVGVPGVGPGAGAGSGAGAGS 60
      |||
Db       1 GAGAGSGAGAGSGVGPVGVPGVGPGKGVPGVGPVGVPGVGPGAGAGSGAGAGS 60
QY      61 GAGAGSGAGAGSGVGPVGVPGVGPGKGVPGVGPVGVPGVGPGAGAGSGAGAGS 120

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: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEO ID NO: 19
: LENGTH: 780
: TYPE: PRT
: ORGANISM: Unknown
: FEATURE:
: OTHER INFORMATION: SEMP 47K
: US-10-939-036-19

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Query Match	100.0%	Score 4173	DB 5	Length 780
Best Local Similarity	100.0%	Pred. NO. 6.6e-248		
Matches 780	0	Mismatches 0	Indels 0	Gaps 0

[illegible]

RESULT 6
US-08-806-029-19
; Sequence 19, Application US/08806029
; Publication No. US20020045567A1
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; APPLICANT: Seddronsky, Erwin R.

TITLE OF INVENTION: Synthetic Proteins for in vivo Drug
 TITLE OF INVENTION: Delivery and Tissue Augmentation
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fleury, Hobbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/806,029
 FILING DATE: 24-FEB-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/212,237
 FILING DATE: 11-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Treccatin, Richard F.
 REGISTRATION NUMBER: 31,801
 REFERENCE/DOCKET NUMBER: A-58847-2/RPT/MTK
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 889 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-806-029-19

Query Match	84.5%	Score 3526;	DB 2;	Length 889;
Best Local Similarity	92.2%;	Pred. No. 2.6e-208;		
Matches 765; Conservative	0;	Mismatches 13;	Indels 52;	Gaps 52

Qy	3	GAGGAGAGAGSvGVPgVgVPgVgPKgKVPgVg - PGVg - PGVg - PGVg - PGVg - PGAGAGSgAGa	58
Db	34	GAGSGAGAGSvGVPgVgVPgVgPKgKVPgVg - PGVg - PGVg - PGVg - PGVg - PGAGAGSgAGa	93
Qy	59	GSgAGAGSgAGAGSgVgVPgVgVPgVgPKgKVPgVg - PGVg - PGVg - PGVg - PGVg - PGAGAGS	114
Db	94	GSgAGAGSgAGAGSgVgVPgVgVPgVgPKgKVPgVg - PGVg - PGVg - PGVg - PGVg - PGAGAGS	153
Qy	115	GAGAGSGAGAGSgAGAGSgVgVPgVgVPgVgPKgKVPgVg - PGVg - PGVg - PGVg - PGVg - PGAGAGS	170
Db	154	GAGAGSGAGAGSgAGAGSgVgVPgVgVPgVgPKgKVPgVg - PGVg - PGVg - PGVg - PGVg - PGAGAGS	213
Qy	171	GAGSGAGAGSgAGAGSgAGAGSgVgVPgVgVPgVgPKgKVPgVg - PGVg - PGVg - PGVg - PGVg - PGAGAGS	227
Db	214	GAGSGAGAGSgAGAGSgAGAGSgVgVPgVgVPgVgPKgKVPgVg - PGVg - PGVg - PGVg - PGVg - PGAGAGS	273
Qy	228	- PGAGAGSgAGAGSgAGAGSgAGAGSgVgVPgVgVPgVgPKgKVPgVg - PGVg - PGVg - PGVg - PGVg - PGAGAGS	283
Db	274	VPGAGAGSgAGAGSgAGAGSgAGAGSgVgVPgVgVPgVgPKgKVPgVg - PGVg - PGVg - PGVg - PGVg - PGAGAGS	333
Qy	284	PGVg - PGAGAGSgAGAGSgAGAGSgAGAGSgVgVPgVgVPgVgPKgKVPgVg - PGVg - PGVg - PGVg - PGVg - PGAGAGS	340
Db	334	PGVgVPgAGAGSgAGAGSgAGAGSgAGAGSgVgVPgVgVPgVgPKgKVPgVg - PGVg - PGVg - PGVg - PGVg - PGAGAGS	393
Qy	341	GVg - PGVg - PGAGAGSgAGAGSgAGAGSgAGAGSgVgVPgVgVPgVgPKgKVPgVg - PGVg - PGVg - PGVg - PGVg - PGAGAGS	397
Db	394	GVgVPgVgVPgAGAGSgAGAGSgAGAGSgAGAGSgVgVPgVgVPgVgPKgKVPgVg - PGVg - PGVg - PGVg - PGVg - PGAGAGS	453
Qy	398	Vg - PGVg - PGVg - PGAGAGSgAGAGSgAGAGSgAGAGSgVgVPgVgVPgVgPKgKVPgVg - PGVg - PGVg - PGVg - PGVg - PGAGAGS	454
Db	454	VgVPgVgVPgVgVPgAGAGSgAGAGSgAGAGSgAGAGSgVgVPgVgVPgVgPKgKVPgVg - PGVg - PGVg - PGVg - PGVg - PGAGAGS	513

Db	694	G V G V G V P G B G P G V G P V G E P E V G V P G A G A G S G A G A G S G A G S G V G V P G	75.3
Oy	679	V G V P E V G P K K V P C V G - P G V G - P G V G - P G A G A S G A G A G S G A G A G S G V	72.4
Db	754	V G V P E V G P G V G P E B G V P G V G P G V G E P G V G P G A G A S G A G A G S G A G S G V	81.3
Oy	735	G V P G V G P G V G P G K G P G V G - P G V G - P G V G - P G V G - P G A G A S G A G A G S	78.0
Db	814	G V P G V G P G V G V G V P G E G V G V G V P G V G E B G V G P G A G A S G A G S	86.3

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RESULT 10
US-10-845-936A-25
; Sequence 25, Application US/10845936A
; Publication No. US20040234609A1
; GENERAL INFORMATION:
; APPLICANT: Collier, Katherine D.
; APPLICANT: Cuevas, William A.
; APPLICANT: Kumar, Manoj A.
; TITLE OF INVENTION: Repeat Sequence Protein Polymer Active Agent Conjugates, Methods
; TITLE OF INVENTION: and Uses
; FILE REFERENCE: DOC0068PA/DC5058/GC792
; CURRENT APPLICATION NUMBER: US/10/845,936A
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: 60/470,464
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 884
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: artificial glycine-rich peptide repeat sequence
US-10-845-936A-25

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[illegible][illegible]

```

RESULT 11
US-10-939-036-25
/ Sequence 25, Application US/10939036
/ Publication No. US20050142094A1
/ GENERAL INFORMATION:
/ APPLICANT: Kumar, Manoj
/ TITLE OF INVENTION: Use of Repeat Sequence Protein Polymers
/ TITLE OF INVENTION: in Personal Care Compositions
/ FILE REFERENCE: GC792-4-2
/ CURRENT APPLICATION NUMBER: US/10/939,036
/ CURRENT FILING DATE: 2004-09-10
/ PRIOR APPLICATION NUMBER: US 10/800,179
/ PRIOR FILING DATE: 2004-03-12
/ PRIOR APPLICATION NUMBER: US 60/454,077
/ PRIOR FILING DATE: 2003-03-12
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: FaalSeq for Windows Version 4.0
/ SEQ ID NO 25
/ LENGTH: 884
/ TYPE: prt
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: SELLP 47E-13
US-10-939-036-25

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Query Match	82.6%	Score 3448	DB 5	Length 884
Best Local Similarity	90.6%	Pred. No. 1.5e+203		
Matches	752	Conservative 0	Mismatches 26	Indels 52
Gaps				52
Qy	3	GAGSGAGAGSGVGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGAGSGAGA	58	
Db	34	GAGSGAGAGSGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGAGAGSGAGA	93	
Qy	59	GSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGAGAGS	114	
Db	94	GSGAGAGSGAGAGSGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGAGAGS	153	
Qy	115	GAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGA	170	
Db	154	GAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGA	213	
Qy	171	GAGSGAGAGSGAGAGSGAGSGVGVPGVGVPGKGVPGVG - PGVG - PGVG - PGVG - PGVG	227	
Db	214	GAGSGAGAGSGAGAGSGAGSGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVG	273	
Qy	228	- PGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG - PGVG - PGVG -	283	
Db	274	VPGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGVPGVGVPGVGVPGVGVPGVG	333	


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FEATURE:
OTHER INFORMATION: silk and elastin and cecropin A melletin peptide repeat sequences
US-10-845-936A-32
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Query Match      82.6%; Score 3448; DB 5; Length 1027;
Best Local Similarity 90.6%; Pred. No. 1.7e-203;
Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;
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QY 3 GAGSAGAGSGSVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 58
DB 177 GAGSAGAGSGSVPGVPGVPGVPGKGVPGVPGVPGVPGVPGVPGVPGVPGV 236
QY 59 GSGAGAGSGAGAGSGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGS 114
DB 237 GSGAGAGSGAGAGSGVPGVPGVPGKGVPGVPGVPGVPGVPGVPGVPGVPGV 296
QY 115 GAGAGSGAGAGSGAGSGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGA 170
DB 297 GAGAGSGAGAGSGAGSGVPGVPGVPGKGVPGVPGVPGVPGVPGVPGVPGV 356
QY 171 GAGSAGAGSGAGAGSGAGSGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG 227
DB 357 GAGSAGAGSGAGAGSGAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 416
QY 228 -PGAGAGSGAGAGSGAGAGSGVPGVPGVPGKGVPGVG-PGVG-PGVG- 283
DB 417 VPGAGAGSGAGAGSGAGAGSGAGSGVPGVPGVPGVPGVPGVPGVPGVPGV 476
QY 284 PGVPG-PGAGAGSGAGAGSGAGAGSGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-P 340
DB 477 PGVPG-PGAGAGSGAGAGSGAGAGSGAGSGVPGVPGVPGVPGVPGVPGKGVPGV 536
QY 341 GVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGSGVPGVPGVPGVPGKGVPGVG-PG 397
DB 537 GVGPGVPGVPGAGAGSGAGAGSGAGAGSGAGSGVPGVPGVPGVPGVPGVPGKGV 596
QY 398 VG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGSGVPGVPGVPGVPGKGVPGV 454
DB 597 VGPVPGVPGVPGAGAGSGAGAGSGAGAGSGAGSGVPGVPGVPGVPGVPGVPGK 656
QY 455 G-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGSGVPGVPGVPGVPGKGV 510
DB 657 GVPVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGSGVPGVPGVPGVPGVPG 716
QY 511 VPGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGSGVPGVPGVPGV 566
DB 717 VPGKGVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGSGVPGVPGVPGV 776
QY 567 PGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGSGVPGV 622
DB 777 PGVPGVPGKGVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGSGVPGV 836
QY 623 GVGPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGSGV 678
DB 837 GVGPGVPGVPGKGVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGSGV 896
QY 679 VGPVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGV 734
DB 897 VGPVPGVPGVPGVPGKGVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGV 956
QY 735 GVPVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGS 780
DB 957 GVPVPGVPGVPGVPGVPGKGVPGVPGVPGVPGVPGVPGVPGVPGAGAGSGAGAGS 1006
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RESULT 14
US-10-845-936A-33
Sequence 33, Application US/10845936A
Publication No. US20040234609A1
GENERAL INFORMATION:
APPLICANT: Collier, Katherine D.
APPLICANT: Cuevas, William A.
APPLICANT: Kumar, Manoj A.
```

```
TITLE OF INVENTION: Repeat Sequence Protein Polymer Active Agent Conjugates, Methods
TITLE OF INVENTION: and Use
FILE REFERENCE: DOC00688PM/DCS058/GC792
CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: 60/470,464
PRIOR FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.2
SEQ ID NO 33
LENGTH: 1105
TYPE: PRT
ORGANISM: unknown
FEATURE:
OTHER INFORMATION: silk, elastin and MBI peptide repeats
US-10-845-936A-33
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Query Match      82.6%; Score 3448; DB 5; Length 1105;
Best Local Similarity 90.6%; Pred. No. 1.8e-203;
Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;
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QY 3 GAGSAGAGSGSVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 58
DB 255 GAGSAGAGSGSVPGVPGVPGVPGKGVPGVPGVPGVPGVPGVPGVPGVPGV 314
QY 59 GSGAGAGSGAGAGSGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGS 114
DB 315 GSGAGAGSGAGAGSGVPGVPGVPGKGVPGVPGVPGVPGVPGVPGVPGVPGV 374
QY 115 GAGAGSGAGAGSGAGSGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGA 170
DB 375 GAGAGSGAGAGSGAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 434
QY 171 GAGSAGAGSGAGAGSGAGSGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG 227
DB 435 GAGSAGAGSGAGAGSGAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 494
QY 228 -PGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 283
DB 495 VPGAGAGSGAGAGSGAGAGSGAGSGVPGVPGVPGVPGVPGVPGVPGVPGV 554
QY 284 PGVPG-PGAGAGSGAGAGSGAGAGSGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-P 340
DB 555 PGVPG-PGAGAGSGAGAGSGAGAGSGAGSGVPGVPGVPGVPGVPGVPGVPGV 614
QY 511 GVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGSGVPGVPGVPGVPGKGVPGVG-PG 397
DB 615 GVGPGVPGVPGAGAGSGAGAGSGAGAGSGAGSGVPGVPGVPGVPGVPGVPGK 674
QY 398 VG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGSGVPGVPGVPGVPGKGV 454
DB 675 VGPVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGSGVPGVPGVPGVPGVPG 734
QY 455 G-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGSGVPGVPGVPGK 510
DB 735 GVPVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGSGVPGVPGVPGVPG 794
QY 511 VPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGSGVPGVPGV 566
DB 795 VPGKGVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGSGVPGVPGVPG 854
QY 567 PGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGSGVPG 622
DB 855 PGVPGVPGKGVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGSGVPGV 914
QY 623 GVGPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGSGV 678
DB 915 GVGPGVPGVPGKGVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGSGV 974
QY 679 VGPVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGV 734
DB 975 VGPVPGVPGVPGVPGKGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 1034
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QY	735	GVPGVGPGVG-PGKGVPGVG-PGVG-PGVG-PGAGSGSAGAGS	780
Db	1035	GVPGVGPVGVP-GVGVGVGKGVPGVGVPGVGPPGAGSGSAGAGS	1084

RESULT 15

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US-10-845-936A-34
: Sequence 34, Application US/10845936A
: Publication No. US20040234609A1
: GENERAL INFORMATION:
: APPLICANT: Collier, Katherine D.
: APPLICANT: Cuevas, William A.
: APPLICANT: Kumar, Manoj A.
: TITLE OF INVENTION: Repeat Sequence Protein Polymer Active Agent Conjugates, Methods
: TITLE OF INVENTION: and Uses
: FILE REFERENCE: DOC068PA/DC058/GC792
: CURRENT APPLICATION NUMBER: US/10/845,936A
: CURRENT FILING DATE: 2004-05-14
: PRIOR APPLICATION NUMBER: 60/470,464
: PRIOR FILING DATE: 2003-05-14
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 34
: LENGTH: 1125
: TYPE: PRT
: ORGANISM: unknown
: FEATURE:
: OTHER INFORMATION: GFP-SELP47K: silk, elastin and green fluorescent protein peptides
US-10-845-936A-34

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Query Match	82.6%	Score 3448	DB 5	Length 1125
Best Local Similarity	90.6%	Pred. No. 1.8e-203		
Matches 752; Conservative	0	Mismatches 26	Indels 52	Gaps 52

[illegible]

QY	567	PGKGVPGVY - PGVY - PGVY - PGVY - PGAGAGSGAGAGSGAGAGSGVGVPGVCP	622
Db	875	PGVGPBGAGVGVGVYPGVGVGVYPPGAGAGSGAGAGSGAGAGSGVGVPGVCP	934
QY	623	GVPGVPGKGVPGV - PGVY - PGVY - PGVY - PGAGAGSGAGAGSGAGAGSGVGVPG	678
Db	935	GVGPBGVYVPGKGVPGVGVPGVGVPGVYPPAGAGSGAGAGSGAGAGSGVGVPG	994
QY	679	VGVPBGVYPGKGVPGVY - PGVY - PGVY - PGVY - PGAGAGSGAGAGSGAGAGSGV	734
Db	995	VGVPBGVYPGVYVPGKGVPGVGVPGVGVPGVYPPAGAGSGAGAGSGAGAGSGV	1054
QY	735	GVPGVYVPGVYVPGKGVPGVY - PGVY - PGVY - PGVY - PGAGAGSGAGAGS	780
Db	1055	GVPGVYVPGVYVPGVYVPGKGVPGVGVPGVGVPGVYPPAGAGSGAGAGS	1104

Search completed: May 10, 2006, 10:48:14
Job time : 171 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2006, 10:45:38 ; Search time 113 Seconds
(without alignments)
324.072 Million cell updates/sec

Title: US-10-800-179-19
Perfect score: 4173
Sequence: 1 GAGAGSGAGAGAGVGVPVG.....GVGPGVPGAGAGSGAGAGS 780

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA New:*
1: /SID55/ptodata/2/pubpaa/US06_NEW_PUB.pep1.*
2: /SID55/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /SID55/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /SID55/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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6: /SID55/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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8: /SID55/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
9: /SID55/ptodata/2/pubpaa/US10_NEW_PUB.pep1.*
10: /SID55/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
11: /SID55/ptodata/2/pubpaa/US11_NEW_PUB.pep1.*
12: /SID55/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3448	82.6	884	11	US-11-201-606-15 Sequence 15, App1
2	2855	68.4	1002	11	US-11-201-606-25 Sequence 25, App1
3	2795	67.0	936	11	US-11-201-606-30 Sequence 30, App1
4	2740	65.7	966	11	US-11-201-606-34 Sequence 34, App1
5	2091.5	50.1	1186	11	US-11-053-100-46 Sequence 46, App1
6	2087.5	50.0	1309	11	US-11-053-100-53 Sequence 53, App1
7	2086	50.0	939	11	US-11-053-100-26 Sequence 26, App1
8	2086	50.0	1174	11	US-11-053-100-43 Sequence 43, App1
9	2086	50.0	1225	11	US-11-053-100-50 Sequence 50, App1
10	2086	50.0	1329	11	US-11-053-100-56 Sequence 56, App1
11	1913.5	45.9	657	11	US-11-053-100-32 Sequence 32, App1
12	1910.5	45.8	639	11	US-11-053-100-25 Sequence 25, App1
13	1910.5	45.8	654	11	US-11-053-100-29 Sequence 29, App1
14	1906.5	45.7	656	11	US-11-053-100-38 Sequence 38, App1
15	1906.5	45.7	657	11	US-11-053-100-35 Sequence 35, App1
16	1904	45.6	874	11	US-11-053-100-42 Sequence 42, App1
17	1429.5	34.3	669	11	US-11-053-100-39 Sequence 39, App1
18	1429.5	34.3	724	11	US-11-053-100-41 Sequence 41, App1
19	1429.5	34.3	879	11	US-11-053-100-55 Sequence 55, App1
20	1428.5	34.2	507	11	US-11-053-100-31 Sequence 31, App1
21	1426	34.2	735	11	US-11-053-100-44 Sequence 44, App1

22	1426	34.2	736	11	US-11-053-100-45	Sequence 45, App1
23	1426	34.2	757	11	US-11-053-100-47	Sequence 47, App1
24	1426	34.2	774	11	US-11-053-100-49	Sequence 49, App1
25	1426	34.2	864	11	US-11-053-100-58	Sequence 58, App1
26	1425	34.1	859	11	US-11-053-100-52	Sequence 52, App1
27	1417.5	34.0	489	11	US-11-053-100-24	Sequence 24, App1
28	1417.5	34.0	504	11	US-11-053-100-28	Sequence 28, App1
29	1415	33.9	506	11	US-11-053-100-37	Sequence 37, App1
30	1415	33.9	507	11	US-11-053-100-34	Sequence 34, App1
31	1411	33.8	775	11	US-11-053-100-51	Sequence 51, App1
32	1411	33.8	879	11	US-11-053-100-57	Sequence 57, App1
33	1367.5	32.8	450	11	US-11-053-100-16	Sequence 16, App1
34	1310	31.4	378	11	US-11-201-606-26	Sequence 26, App1
35	1119.5	26.8	574	11	US-11-053-100-40	Sequence 40, App1
36	1118.5	26.8	357	11	US-11-053-100-30	Sequence 30, App1
37	1107.5	26.5	339	11	US-11-053-100-23	Sequence 23, App1
38	1107.5	26.5	354	11	US-11-053-100-27	Sequence 27, App1
39	1105	26.5	356	11	US-11-053-100-36	Sequence 36, App1
40	1105	26.5	357	11	US-11-053-100-33	Sequence 33, App1
41	1096	26.3	1901	11	US-11-052-554A-135	Sequence 135, App
42	1089.5	26.1	1079	11	US-11-052-554A-145	Sequence 145, App
43	1034	24.8	1660	11	US-11-052-554A-137	Sequence 137, App
44	1021	24.5	624	11	US-11-053-100-48	Sequence 48, App
45	1021	24.5	728	11	US-11-053-100-54	Sequence 54, App1

ALIGNMENTS

RESULT 1
US-11-201-606-15
; Sequence 15, Application US/11201606
; Publication NO. US20060029638A1
; GENERAL INFORMATION:
; APPLICANT: STEDRONSKY, Erwin R.
; TITLE OF INVENTION: Tissue Adhesive Using Synthetic
; TITLE OF INVENTION: Crosslinking
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
; STREET: Four Embarcadero Center, Suite 200
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/201,606
; FILING DATE: 2005-08-10
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/642,246
; FILING DATE: 1996-05-02
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ROWLAND, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A61127-1/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 884 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide


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; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 936 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
;
US-11-201-606-30

Query Match      67.0%; Score 2795; DB 11; Length 936;
Beet Local Similarity 73.9%; Pred. No. 4,1e-185;
Matches 642; Conservative 4; Mismatches 93; Indels 130; Gaps 55

QY      1  GAGAGSGAGAGSGVGV-----PGVGPVGVPVPKGVPGVG- PGYG- PGYG- PGYG- PGA 50
Db      92  GAGAGSGAGAGSGVGPLG-PLGPGVGPVGVPVGVPKGVPGVGVPAGVPGVGA 151
QY      51  GAGAGGAGAGSGAGAGSGAGAGSGVGVPGVPGVPGKGVPGVPGVPGYG- PGYG- P 108
Db     152  GAGGAGAGAGSGVGPLG-PLGPGVPGVPGVPGVPGKGVPGVG---PGVGVPGVGP 207
QY     109  GAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVPGVPGKGVPGVPGVPGYG- PGYG 167
Db     208  GAGAGSGAGAGSGVGPLG-PLGPGVPGVPGVPGVPGKGVPGVG---PGVGPVGG 263
QY     168  -PGAAGSGAGAGSGAGAGSGAGAGSGVGVPGVPGVPGKGVPGVPGVPGYG- PG 225
Db     264  VPGAAGSGAGAGSGVGPLG-PLGPGVPGVPGVPGVPGKGVPGVG---PGVGPBG 319
QY     226  VG- PGAGAGSGAGAGSGAGAGSGAGAGSGVGPVPGVPGVPGKGVPGVPGYG- PGYG- 283
Db     320  VGVPGAGAGSGAGAGSGVGPLG-PLGPGVPGVPGVPGVPGKGVPGVG---PGVGP 375
QY     284  PGVG- PGAAGSGAGAGSGAGAGSGAGAGSGVGPVPGVPGVPGKGVPGVPGVPGYG 342
Db     376  PGVGPAGAAGSGAGAGSGVGPLG-PLGPGVPGVPGVPGVPGKGVPGVG---PGV 431
QY     343  G-PGVG- PGAAGSGAGAGSGAGAGSGAGAGSGVGPVPGVPGVPGKGVPGVPGYG 400
Db     432  GVPVGPVPGAAGSGAGAGSGVGPLG-PLGPGVPGVPGVPGVPGKGVPGVG---P 487
QY     401  GVG- PGVG- PGAAGSGAGAGSGAGAGSGAGAGSGVGPVPGVPGVPGKGVPGVPGYG 458
Db     488  GVGVPVGPVPGAAGSGAGAGSGVGPLG-PLGPGVPGVPGVPGVPGKGVPGVG--- 544
QY     459  GPVG- PGVG- PGAAGSGAGAGSGAGAGSGAGAGSGVGPVPGVPGVPGKGVPGVPG 516
Db     545  -PGVGPVPGVPGAAGSGAGAGSGVGPLG-PLGPGVPGVPGVPGVPGKGVPGVG 602
QY     517  GVGPGVG- PGVG- PGAAGSGAGAGSGAGAGSGAGAGSGVGPVPGVPGVPGKGVPG 574
Db     603  ---PGVGPVPGVPGAAGSGAGAGSGVGPLG-PLGPGVPGVPGVPGVPGKGVPG 658
QY     575  GPVGVPVG- PGVG- PGAAGSGAGAGSGAGAGSGAGAGSGVGPVPGVPGVPGKGV 632
Db     659  GV---PGVGPVPGVPGAAGSGAGAGSGVGPLG-PLGPGVPGVPGVPGVPGKGV 714
QY     633  GVGPGVPGVG- PGVG- PGAAGSGAGAGS----- 660
Db     715  GVGV---PGVGPVPGVPGAAGSGAGAGSGVGPLG-PLGPGVPGVPGVPGVPGKGV 771
QY     661  -----GAGAGSGAGAGSGVG---PGVGPVPGVPGKGVPGVG- PG 697
Db     772  PGVGPVPGVPGVPGAAGSGAGAGSGVGPLG-PLGPGVPGVPGVPGVPGKGVPG 831
QY     698  VG- PGVG- PGVG- PGAAGSGAGAGSGAGAGSGAGAGSGVGPVPGVPGVPGKGVPG 754
Db     832  VGVGPVGPVPGAAGSGAGAGSGVGPLG-PLGPGVPGVPGVPGVPGKGVPGV 890
QY     755  G-PGVG- PGVG- PGVGPAGAAGSGAGAGS 780
Db     891  GVPVGPVPGVPGAAGSGAGAGSGAGAGSAGA 919

```


Db 6 GPGVGVPGVPGGGVPGAGVPGVGVPGVPGGGVPGAGVPGGGVPGVGVPGVG 65
Qy 60 SGAGAGSAGAGAGSAGVPGVGVPGVGVPGKGVPGVG-----PGVG-PGVG----- 103
Db 66 VPGGGVPGAGV-PGVGVPGVGVPGGGVPGAGVPGGGVPGGGVPGGGVPGGA 124
Qy 104 --PGVG-PGAGA-GSAGAGSAGAGSAGSAGVPGVPGVPGVPGKGVPGVG-PGV 158
Db 125 GVPGVGVPGVGVPGGVPGGGVPGAGVPGGGVPGGVPGGGVPGAGVPGGVPGV 184
Qy 159 G-PGVG-PGVG-PGAGAGSAG-----GAGSAGAGSAGAGSAGVPGVPGVPGVG 208
Db 185 GVPGVGVPGGGVPGAGVPGGGVPGGVPGVPGGGVPGAGV-PGVGVPGVPGVPG 243
Qy 209 KGVPGVG-----PGVG-PGVG-----PGVG-PGAGA-GSAGAGSAGAGSAG 248
Db 244 GGVPGAGVPGGGVPGGVPGGVPGGGVPGAGVPGGVPGGVPGGGVPGAGVPG 303
Qy 249 GAGSAGVPGVGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSAG-----G 297
Db 304 GGVPGVGVPGVPGGGVPGAGVPGGVPGGVPGGGVPGGGVPGGGVPGGVPG 363
Qy 298 AGSAGAGSAGAGSAGSAGVPGVPGVPGKGVPGVG-----PGVG-PGVG----- 343
Db 364 VGVPGGGVPGAGV-PGVGVPGVGVPGGVPGGGVPGAGVPGGGVPGGVPGGGV 422
Qy 344 ----PGVG-PGAGA-GSAGAGSAGAGSAGAGSAGVPGVPGVPGVPGKGVPGVG-P 396
Db 423 GAGVPGVGVPGVGVPGGGVPGAGVPGGGVPGGVPGGVPGGGVPGAGVPGVGP 482
Qy 397 GVG-PGVG-PGVG-PGAGAGSAGAGSAG-----GAGSAGAGSAGVPGVPGVPGKGV 452
Db 483 GVGVPGVGVPGGGVPGAGVPGGGVPGGVPGGGVPGAGVPGGVPGGVPGVGVP 542
Qy 453 GVG-PGVG-PGVG-PGAGAGSAGAGSAGAGSAGAG-----SGVGVPGVGVPGVGP 507
Db 543 GGGVPGAGVPGGGVPGGVPGGGVPGGGVPGAGVPGGVPGGVPGGGVPGAGV 602
Qy 508 GKGVPGVG-PGVG-----PGVG-PGVG-PGAGA-GSAGAGSAGAGSAGAGSAGV 557
Db 603 GGGVPGVGVPGGVPGGGVPGAGVPGGVPGGVPGGVPGGGVPGAGVPGGVGP 662
Qy 558 GVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGAGAGSAGAGSAG-----G 297
Db 663 GVGVPGGVPGAGVPGVPGGVPGGVPGGGVPGAGVPGGGVPGGVPGGGV 722
Qy 613 GVGVPGVGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSAGAGSAGAGSAG 668
Db 723 GAGVPGVGVPGVPGVPGGGVPGAGVPGGGVPGGVPGGGVPGAGVPGVGP 782
Qy 669 GAG-SGVGVPGVPGVPGKGVPGVG-PGVG-----PGVG-PGVG-PGAGA-GSAG 717
Db 783 GVGVPGVGVPGGGVPGAGVPGGGVPGGVPGGVPGGGVPGAGVPGGVPGVGP 842
Qy 718 AGSAGAGSAGAGSAGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGAGA- 772
Db 843 GGGVPGAGVPGGGVPGGVPGGVPGGGVPGAGVPGVPGVPGGVPGGGVPGAGV 902
Qy 773 -----GSGAGAGS 780
Db 903 GGGVPGWPSGGGGGS 918

RESULT 6
US-11-053-100-53
; Sequence 53, Application US/11053100
; Publication No. US20050255554A1
; GENERAL INFORMATION:
; APPLICANT: CHIKORI, Ashutosh
; TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
; FILE REFERENCE: 4176-101 CIP
; CURRENT APPLICATION NUMBER: US/11/053,100
; CURRENT FILING DATE: 2005-02-08

; PRIOR APPLICATION NUMBER: US 09/812,382
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,659
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 53
; LENGTH: 1309
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(1309)
; OTHER INFORMATION: PET15b-SD1-ELP1-180-throm-G protein alpha Q
; US-11-053-100-53

Query Match 50.0%; Score 2087.5; DB 11; Length 1309;
Best Local Similarity 59.2%; Pred. No. 1.7e-136; Indels 147; Gaps 68;
Matches 541; Conservative 3; Mismatches 223;

Qy 11 GSGVGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSAG-----GAG 59
Db 6 GPGVGVPGVPGGGVPGAGVPGGVPGVPGGGVPGAGVPGGGVPGGVPGGGVPG 65
Qy 60 SGAGAGSAGAGSAGSAGVPGVPGVPGKGVPGVG-----PGVG-PGVG----- 103
Db 66 VPGGGVPGAGV-PGVGVPGVGVPGGGVPGAGVPGGGVPGGGVPGGGVPGGA 124
Qy 104 --PGVG-PGAGA-GSAGAGSAGAGSAGAGSAGVPGVPGVPGVPGKGVPGVG-PGV 158
Db 125 GVPGVGVPGVGVPGGGVPGAGVPGGGVPGGVPGGGVPGAGVPGGVPGVPGV 184
Qy 159 G-PGVG-PGVG-PGAGAGSAG-----GAGSAGAGSAGAGSAGVPGVPGVPGVG 208
Db 185 GVPGVGVPGGGVPGAGVPGGGVPGGVPGGVPGGGVPGAGV-PGVGVPGVPGVG 243
Qy 209 KGVPGVG-----PGVG-PGVG-----PGVG-PGAGA-GSAGAGSAGAGSAG 248
Db 244 GGVPGAGVPGGGVPGAGVPGGGVPGGVPGGVPGGGVPGAGVPGGGVPGAGV 303
Qy 249 GAGSAGVPGVGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSAG-----G 297
Db 304 GGVPGVGVPGGVPGGGVPGAGVPGGGVPGGVPGGGVPGAGVPGGGVPGVG 363
Qy 298 AGSAGAGSAGAGSAGSAGVPGVPGVPGKGVPGVG-----PGVG-PGVG----- 343
Db 364 VGVPGGGVPGAGV-PGVGVPGVGVPGGGVPGAGVPGGGVPGGVPGGGVPGAGV 422
Qy 344 ----PGVG-PGAGA-GSAGAGSAGAGSAGAGSAGVPGVPGVPGVPGKGVPGVG-P 396
Db 423 GAGVPGVGVPGVPGVPGGGVPGAGVPGGGVPGGVPGGVPGGGVPGAGVPGVGP 482
Qy 397 GVG-PGVG-PGVG-PGAGAGSAGAGSAG-----GAGSAGAGSAGVPGVPGVPGKGV 452
Db 483 GVGVPGVGVPGGGVPGAGVPGGGVPGGVPGGVPGGGVPGAGVPGGVPGVGP 542
Qy 453 GVG-PGVG-PGVG-PGAGAGSAGAGSAGAGSAGAG-----SGVGVPGVGVPGVGP 507
Db 543 GGGVPGAGVPGGGVPGGVPGGVPGGGVPGAGVPGGGVPGGVPGGGVPGAGV 602
Qy 508 GKGVPGVG-PGVG-----PGVG-PGVG-PGAGA-GSAGAGSAGAGSAGAGSAGV 557
Db 603 GGGVPGVGVPGVPGGGVPGAGVPGGVPGGVPGGVPGGGVPGAGVPGGGVPGVGP 662
Qy 558 GVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGAGAGSAGAGSAG-----GAGSAGAGS 612
Db 663 GVGVPGGVPGAGVPGVPGVPGVPGGGVPGAGVPGGGVPGGVPGGVPGVPGGGV 722
Qy 613 GVGVPGVGVPGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSAGAGSAGAGSAG 668
Db 723 GAGVPGVGVPGVPGVPGGGVPGAGVPGGGVPGGVPGGVPGGGVPGAGVPGVGP 782

QY		663	GAG-SSGVPGVGPBVGVPBGKGVPEVG-PGVG-----PVG-PGVG-PGAQA-GSQAQ	717
Db		783	GGVPPGVGPBGSGVPGAAGVPGGGVPGVG/PBGVPGGGVPGAAGVPGVGPBGVPGV	842
QY		718	AGSGAAGSGAGAAGSGVGPVGVP/VPGV/PBGKVPEVG-PGVG-PGVG-PGAAG	773
Db		843	GGGVPGAAGVPGGGVPGVG/PBGV/PBGCGVPGAAGVPGVGPBGV/PBGGGVGAAGV	902
QY		774	SG-----AGAGS	780
Db		903	GGGVPGMFPSSGGGS	916
RESULT 7				
		US-11-053-100-26		
		/ Sequence 26, Application US/11053100		
		/ Publication No. US2005025554A1		
		/ GENERAL INFORMATION:		
		/ APPLICANT: CHILIKOTI, Ashutosh		
		/ TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION		
		/ FILE REFERENCE: 4176-101 CIP		
		/ CURRENT APPLICATION NUMBER: US/11/053,100		
		/ CURRENT FILING DATE: 2005-02-08		
		/ PRIOR APPLICATION NUMBER: US 09/812,382		
		/ PRIOR FILING DATE: 2001-03-20		
		/ PRIOR APPLICATION NUMBER: US 60/190,659		
		/ PRIOR FILING DATE: 2000-03-20		
		/ SOFTWARE: PatentIn version 3.3		
		/ NUMBER OF SEQ ID NOS: 58		
		/ SEQ ID NO 26		
		/ LENGTH: 939		
		/ TYPE: PRt		
		/ ORGANISM: Artificial		
		/ FEATURE:		
		/ OTHER INFORMATION: Synthetic Construct		
		/ FEATURE:		
		/ NAME/KEY: MISC FEATURE		
		/ LOCATION: (11)-(939)		
		/ OTHER INFORMATION: PET32a-SDI5-ELF1-180-EK-Inseulin A peptide		
		US-11-053-100-26		
Query Match				
		Best Local Similarity	50.0%; Score 2086; DB 11; Length 939;	
		Matches	539; Conservative 2; Mismatches 225; Indels 140; Gaps 67	
QY		11	GSAGVGPVGVPVGVPBGKVPBGV-PGVG-PGVG-PGVG-PGAAGSA-----GAG	59
Db		3	GPVGVPBGVPGGGVPGAAGVPGVGPBGV/PBGV/PBGAGVPGAAGVPGGGVPGVGPVG	62
QY		60	SGAGASSGAGASGSGVGPVGVPVGPKGVPGVG-----PGVG-PGVG-----	103
Db		63	VPGGVPBGAGV-PGVGPBGVPGVGPVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGA	121
QY		104	--PGVG-PGAQA-GSAGAGSSGAGASGAGSGVGPVGVPVGVPBGKVPBGV-PGV	158
Db		122	GVPGVGPVGVPVGVPVPGGVPGAAGVPGAAGVPGVGPBGVPGAAGVPGAAGVPGAAGV	181
QY		159	G-PGVG-PGVG-PGAAGSA-----GAGSAGAGSAGAGSGVGPVGVPBG	208
Db		182	GVPGVGPVGAGVPGAAGVPGAAGVPGVGPBGVPGAAGVPGAAGVPGAAGVPGAAGVPGA	240
QY		209	KGVPGV-----PGVG-PGVG-----PGVG-PGAQA-GSAGAGSAGAGSA	248
Db		241	GGVPGAAGVPGGGVPGVGPBGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGV	300
QY		249	GAGSGVGPBGVGPVGVPBGKVPBGV-PGVG-PGVG-PGVG-PGAAGSA-----G	297
Db		301	GGVGPVGVPBGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGV	360
QY		298	AGSGAAGSAGAGSGVGPVGVPBGV/PBGKVPEVG-----PGVG-PVG-----	343
Db		361	VGPBGAGVPGAAGV-PGVGPBGVGPVGVPBGGGVPGAAGVPGAAGVPGAAGVPGAAGV	419

QY		344	-----PENV-PGAG-GSAGAGSGAGAGSGAGSGAGSGVCPGVGVPGVCVPBGKGPVG-V-P	396
Db		420	GAGVPGVGVPEVGVPGVGVPCGGVPGAAGVPCGGVPGVGVPEVGVPCGGVPGAAGVPGAAGV	479
QY		397	GVG--PGV--PGV--PGAAGAGSGAGAAGSGA--GAGSGAGAGSGVGVPGVGVPGKGV	452
Db		480	GVGVPGVGVPEGGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGV	539
QY		453	GVG--PGV--PGV--PGV--PGAAGAGSGAGAGSGAGAGAG--SGVGVPGVGVPGVGV	507
Db		540	GAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGV	599
QY		508	GKVPDGV--PGV-----PGV--PGV--PGAAG-GSAGAGSGAGAGSGAGSGAGSVGV	557
Db		600	GAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGV	659
QY		558	GVGVPGVGVPEKGVPAGV--PGV--PGV--PGAAGAGSGAGAAGSGA--GAGSGAGAGS	612
Db		660	GVGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGV	719
QY		613	GVGVPGVGVPEGVPGKVPVG--PGV--PGV--PGV--PGAAGAGSGAGAGSGAGAGSGA	668
Db		720	GAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGV	779
QY		669	GAG--SGVGVPGVGVPGVPGKVPVG--PGV-----PGV--PGV--PGAAG-GSAG	717
Db		780	GVGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGV	839
QY		718	AGSGAGAGSGAGAGSGAGVPGVPGVPGVPGKVPVG--PGV--PGV--PGAAG-PAAG	773
Db		840	GAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGV	899
QY		774	SGAGAG 779	
Db		900	GAGVPG 905	
RESULT 8				
US-11-053-100-43				
; Sequence 43, Application US/11053100				
; Publication No. US2005025554A1				
; GENERAL INFORMATION:				
; APPLICANT: CHIKORI, Ashutosh				
; TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION				
; FILE REFERENCE: 4176-101 CIP				
; CURRENT APPLICATION NUMBER: US/11/053,100				
; CURRENT FILING DATE: 2005-02-08				
; PRIOR APPLICATION NUMBER: US 09/812,382				
; PRIOR FILING DATE: 2001-03-20				
; PRIOR APPLICATION NUMBER: US 60/190,659				
; PRIOR FILING DATE: 2000-03-20				
; NUMBER OF SEQ ID NOS: 58				
; SOFTWARE: PatentIn version 3.3				
; SEQ ID NO 43				
; LENGTH: 1174				
; TYPE: PRT				
; ORGANISM: Artificial				
; FEATURE:				
; OTHER INFORMATION: Synthetic Construct				
; FEATURE:				
; NAME/KEY: MISC FEATURE				
; LOCATION: (1) ..(1174)				
; OTHER INFORMATION: pet15b-SDS-ELPI-180-throm-Tobacco etch virus protease				
US-11-053-100-43				
Query Match 50.0%, Score 2086, DB 11, Length 1174;				
Best Local Similarity 59.5%, Pred. No. 2e-136;				
Matches 539; Conservative 2; Mismatches 225; Indels 140; Gaps 67;				
QY		11	GSAGVPGVGVPGVGVPGKGVPGV--PGV--PGV--PGAAGAGSGA-----GAG	59
Db		6	GPAGVPGVGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGVPGAAGV	65

QY 60 SGAGAGSAGAGSGVPGVPGKGVPGV-----PGVG-PGVG----- 103
DB 66 VPGGAGVPGAGV-PGVGPGVPGVPGGAGVPGAGVPGGAGVPGVPGGAGVPGA 124
QY 104 --PGVG-PGAGA-GSAGAGSAGAGSAGAGSGVPGVPGVPGKGVPGVG-PGV 158
DB 125 GVPBGVPGVPGVPGVPGGAGVPGAGVPGGAGVPGVPGGAGVPGAGVPGV 184
QY 159 G-PGVG-PGAGA-PGAGAGSGA-----GAGSAGAGSAGAGSGVPGVPGV 208
DB 185 GVPBGVPGGAGVPGAGVPGGAGVPGAGVPGVPGGAGVPGAGV-PGVGPGVPGV 243
QY 209 KGVPGV-----PGVG-PGVG-----PGVG-PGAGA-GSAGAGSAGAGS 248
DB 244 GGVPGAGVPGGAGVPGVPGVPGGAGVPGAGVPGVPGVPGVPGGAGVPGA 303
QY 249 GAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSGA-----G 297
DB 304 GGVPGVPGVPGGAGVPGAGVPGVPGVPGGAGVPGAGVPGGAGVPGVPG 363
QY 298 AGSAGAGSAGAGSGVPGVPGVPGKGVPGVG-----PGVG-PGVG----- 343
DB 364 VGVPGGAGVPGAGV-PGVGPGVPGVPGGAGVPGAGVPGGAGVPGVPGGAGV 422
QY 344 ----PGVG-PGAGA-GSAGAGSAGAGSAGAGSGVPGVPGVPGKGVPGVG-P 396
DB 423 GAGVPGVPGVPGVPGVPGGAGVPGGAGVPGGAGVPGVPGGAGVPGAGV 482
QY 397 GVG-PGVG-PGAGA-GSAGAGSAGAGSGA-GAGSAGAGSGVPGVPGVPGK 452
DB 483 GGVPGAGVPGGAGVPGGAGVPGGAGVPGGAGVPGGAGVPGGAGVPGV 542
QY 453 GVG-PGVG-PGVG-PGAGAGSAGAGSAGAGSAGAG-SGVPGVPGVPGV 507
DB 543 GGVPGAGVPGGAGVPGVPGGAGVPGGAGVPGGAGVPGVPGGAGVPGA 602
QY 508 GKVPGVG-PGVG-----PGVG-PGAGA-GSAGAGSAGAGSAGAGSGV 557
DB 603 GGVPGVPGVPGVPGGAGVPGAGVPGVPGVPGGAGVPGGAGVPGAGV 662
QY 558 GVPBGVPGVPGVPGVPGV-PGVG-PGVG-PGAGAGSAGAGSAGAGSAG 612
DB 663 GGVPGGAGVPGAGVPGVPGVPGGAGVPGAGVPGGAGVPGVPGGAGV 722
QY 613 GVPBGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSAGAGSAGAGS 668
DB 723 GAGVPGVPGVPGVPGVPGGAGVPGAGVPGGAGVPGGAGVPGAGV 782
QY 669 GAG-SGVPGVPGVPGVPGKGVPGVG-PGVG-----PGVG-PGAGA-GSAG 717
DB 783 GVPBGVPGGAGVPGAGVPGGAGVPGVPGGAGVPGAGVPGVPGVPGV 842
QY 718 AGSAGAGSAGAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAG 773
DB 843 GGVPGAGVPGGAGVPGVPGGAGVPGAGVPGVPGVPGVPGGAGVPGA 902
QY 774 SGAGAG 779
DB 903 GGVPG 908

RESULT 9
US-11-053-100-50
; Sequence 50, Application US/11053100
; Publication No. US2005025554A1
; GENERAL INFORMATION:
; APPLICANT: CHIKORI, Ashutosh
; TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
; FILE REFERENCE: 4176-101 CIP
; CURRENT APPLICATION NUMBER: US/11/053.100
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 09/812,382

QY 11 GSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSGA-----GAG 59
DB 6 GPGVPGVPGVPGGAGVPGAGVPGVPGVPGGAGVPGAGVPGGAGVPGVPG 65
QY 60 SGAGAGSAGAGSGVPGVPGVPGKGVPGVG-----PGVG-PGVG----- 103
DB 66 VPGGAGVPGAGV-PGVGPGVPGVPGGAGVPGAGVPGGAGVPGVPGGAGVPGA 124
QY 104 --PGVG-PGAGA-GSAGAGSAGAGSAGAGSGVPGVPGVPGKGVPGVG-PGV 158
DB 125 GVPBGVPGVPGVPGVPGGAGVPGAGVPGGAGVPGVPGGAGVPGAGVPGV 184
QY 159 G-PGVG-PGAGA-PGAGAGSGA-----GAGSAGAGSAGAGSGVPGVPGV 208
DB 185 GVPBGVPGGAGVPGAGVPGGAGVPGAGVPGVPGGAGVPGAGV-PGVGPGVPGV 243
QY 209 KGVPGV-----PGVG-PGVG-----PGVG-PGAGA-GSAGAGSAGAGS 248
DB 244 GGVPGAGVPGGAGVPGVPGVPGGAGVPGAGVPGGAGVPGGAGVPGAGV 303
QY 249 GAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSGA-----G 297
DB 244 GGVPGAGVPGGAGVPGVPGGAGVPGGAGVPGGAGVPGGAGVPGAGV 303
QY 209 G-PGVG-PGVG-PGAGAGSAGAGSAGAGSAGAG-SGVPGVPGVPGV 507
DB 543 GGVPGAGVPGGAGVPGVPGGAGVPGGAGVPGGAGVPGGAGVPGA 602
QY 508 GKVPGVG-PGVG-----PGVG-PGAGA-GSAGAGSAGAGSAGAGSGV 557
DB 603 GGVPGVPGVPGVPGGAGVPGAGVPGGAGVPGVPGGAGVPGAGVPGVPGV 662
QY 558 GVPBGVPGVPGVPGVPGV-PGVG-PGVG-PGAGAGSAGAGSAGAGSAG 612
DB 663 GGVPGGAGVPGAGVPGVPGVPGGAGVPGAGVPGGAGVPGVPGGAGVPGA 722
QY 613 GVPBGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSAGAGSAGAGS 668
DB 723 GAGVPGVPGVPGVPGGAGVPGAGVPGGAGVPGAGVPGVPGGAGVPGA 782

QY 11 GSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSGA-----GAG 59
DB 6 GPGVPGVPGVPGGAGVPGAGVPGVPGVPGGAGVPGAGVPGGAGVPGVPG 65
QY 60 SGAGAGSAGAGSGVPGVPGVPGKGVPGVG-----PGVG-PGVG----- 103
DB 66 VPGGAGVPGAGV-PGVGPGVPGVPGGAGVPGAGVPGGAGVPGVPGGAGVPGA 124
QY 104 --PGVG-PGAGA-GSAGAGSAGAGSAGAGSGVPGVPGVPGKGVPGVG-PGV 158
DB 125 GVPBGVPGVPGVPGVPGGAGVPGAGVPGGAGVPGVPGGAGVPGAGVPGV 184
QY 159 G-PGVG-PGAGA-PGAGAGSGA-----GAGSAGAGSAGAGSGVPGVPGV 208
DB 185 GVPBGVPGGAGVPGAGVPGGAGVPGAGVPGVPGGAGVPGAGV-PGVGPGVPGV 243
QY 209 KGVPGV-----PGVG-PGVG-----PGVG-PGAGA-GSAGAGSAGAGS 248
DB 244 GGVPGAGVPGGAGVPGVPGVPGGAGVPGAGVPGGAGVPGGAGVPGAGV 303
QY 249 GAGSGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSGA-----G 297
DB 244 GGVPGAGVPGGAGVPGVPGGAGVPGGAGVPGGAGVPGGAGVPGAGV 303
QY 209 G-PGVG-PGVG-PGAGAGSAGAGSAGAGSAGAG-SGVPGVPGVPGV 507
DB 543 GGVPGAGVPGGAGVPGVPGGAGVPGGAGVPGGAGVPGGAGVPGA 602
QY 508 GKVPGVG-PGVG-----PGVG-PGAGA-GSAGAGSAGAGSAGAGSGV 557
DB 603 GGVPGVPGVPGVPGGAGVPGAGVPGGAGVPGVPGGAGVPGAGVPGVPGV 662
QY 558 GVPBGVPGVPGVPGVPGV-PGVG-PGVG-PGAGAGSAGAGSAGAGSAG 612
DB 663 GGVPGGAGVPGAGVPGVPGVPGGAGVPGAGVPGGAGVPGVPGGAGVPGA 722
QY 613 GVPBGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGAGAGSAGAGSAGAGS 668
DB 723 GAGVPGVPGVPGVPGGAGVPGAGVPGGAGVPGAGVPGVPGGAGVPGA 782

Query Match 50.0%; Score 2086; DB 11; Length 1225;
Best Local Similarity 59.5%; Pred. No. 2, 1e-136;
Matches 539; Conservative 2; Mismatches 225; Indels 140; Gaps 67;

Qy	669	GAG-SGVGVPGVGVGVPGKGVPGV--PGV-----PGV-PGV-PGAG--GSAG	717
Db	783	GVGVPGVGVPGGGVPGAGVPGGGVPGVPGAGVPGVGVPGVGP	842
Qy	718	AGSGAGAGSAGAGSGVGVPGVGVPGVPGKGVPGV--PGV-PGV-PGV-PGAG	773
Db	843	GGGVPGAGVPGGGVPGVGVPGVPGGGVPGAGVPGVGVPGVGPVGGVPGAGVP	902
Qy	774	SGAG	779
Db	903	GGGVPG	908

```

RESULT 10
US-11-053-100-56
; Sequence 56, Application US/11053100
; Publication No. US20050255554v1
; GENERAL INFORMATION:
; APPLICANT: CHILKOTI, Ashutosh
; TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
; FILE REFERENCE: 4176-101 CIP
; CURRENT APPLICATION NUMBER: US/11/053,100
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 09/812,382
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,659
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56
; LENGTH: 1329
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)_(1329)
; OTHER INFORMATION: PET15b-SN5-ELP1.180-throm-1-Deoxy-D-Xyulose 5-Phosphate
; US-11-053-100-56

```

Query Match	50.0%;	Score 2086;	DB 11;	Length 1329;
Best Local Similarity	59.5%;	Pred. No. 2.2e-136;		
Matches 539; Conservative	2;	Mismatches 225;	Indels 140;	Gaps 67;

OY	1	SSGVCVPGVGVGVGVPGKGVPGV- -PGV- -PGV- -PGV- -PGAGAGSA-----GAG	59
Db	6	GPVGVPVGVPGGGVPGAGVPGVGPVGVPVGVPVGAGVPGGGVPGVGPVG	65
OY	60	SGAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGV-----PGV- -PGV-----	103
Db	66	VPGGVPAGAV- -PGVGPVGVPVGVPVGPGGVPAGAVPGGVPVGVPVGVPGGVPAG	124
OY	104	--PGV- -PGAG- -GSGAGAGSGAGAGSGVGPVGVPVGVPVGKGVPGV- -PGV	158
Db	125	GVPGVPVGVPVGVPVGVPVGAGVPGGVPVGVPVGVPVGVPGGVPAGGVPGVGPV	184
OY	159	G- -PGV- -PGV- -PGAGAGSGA-----GAGAGAGSGAGAGSGVGPVGVPVGVP	208
Db	185	GVPGVPVGVPVGAGVPGGVPVGVPVGVPGGGVPAGV- -PGVGPVGVPVGVPVG	243
OY	209	KGVPVG-----PGV- -PGV-----PGV- -PGAG- -GSGAGAGSGAGAGSGA	248
Db	244	GGVPAGVPGGVPVGVPVGVPVGVPGGGVPAGVPVGVPVGVPVGVPGGGVPAGAVPG	303
OY	249	GAGSGVPVGVPVGVPVGKGVPGV- -PGV- -PGV- -PGV- -PGAGAGSGA-----G	297
Db	304	GGVPVGVPVGVPVGAGVPVGVPVGVPVGVPVGCGGVPAGAVPGGVPVGVPVG	363
OY	298	AGSGAGAGSGAGSGVGPVGVPVGVPVGKGVPGV-----PGV- -PGV-----	343
Db	364	VGPVGGPVGAV- -PGVGPVGVPVGVPVGVPAGVPGGGVPVGVPVGVPVGVP	422

QY	344	----	PGVG	-PGAGA	-GSGAGAGS	GAGAGS	GAGAGS	GVGVP	PGKGV	PGVG	-P	336
Db	423	GAGV	PGVGV	PGVGV	PGVGV	PGAGV	PGGGV	PGVGV	PGVGV	PGGGV	PGAGV	PGVGV
QY	397	GVG	-PGVG	-PGVG	-PGAGAGS	GAGAGS	GGA	-GAGS	GAGAGS	GVGVP	PGVGV	PGKGV
Db	483	GVG	PGVGV	PGGGV	PGAGV	PGGGV	PGVGV	PGVGV	PGGGV	PGAGV	PGVGV	PGVGV
QY	453	GVG	-PGVG	-PGVG	-PGAGAGS	GAGAGS	GAGAGS	GAGAG	-SGVGV	PGVGV	PGVGV	507
Db	543	GGGV	PGAGV	PGGGV	PGVGV	PGGGV	PGAGV	PGVGV	PGVGV	PGGGV	PGAGV	6022
QY	508	GKGV	PGVG	-PGVG	-----	PGVG	-PGVG	-PGAGA	-GSGAGAGS	GAGAGS	GVGVP	557
Db	603	GGGV	PGVGV	PGGGV	PGAGV	PGVGV	PGGGV	PGAGV	PGGGV	PGAGV	PGGGV	6622
QY	558	GVG	VG	VG	VG	VG	VG	VG	VG	VG	VG	612
Db	663	GVG	VG	PGGGV	PGAGV	PGVGV	PGGGV	PGAGV	PGGGV	PGVGV	PGGGV	722
QY	613	GVG	VG	PGVGV	PGKGV	PGVG	-PGVG	-PGVG	-PGAGAGS	GAGAGS	GAGAGS	668
Db	723	GAGV	PGVGV	PGGGV	PGAGV	PGGGV	PGVGV	PGVGV	PGGGV	PGAGV	PGVGV	782
QY	669	GAG	-SGVG	PGVGV	PGVGV	PGKGV	PGVG	-PGVG	-----	PGVG	-PGVG	717
Db	783	GVG	VG	PGVGV	PGGGV	PGAGV	PGGGV	PGVGV	PGGGV	PGAGV	PGVGV	842
QY	718	AGS	GAGAGS	GAGAGS	GVGVP	PGVGV	PGVGV	PGKGV	PGVG	-PGVG	-PGVG	773
Db	843	GGGV	PGAGV	PGGGV	PGVGV	PGVGV	PGGGV	PGAGV	PGVGV	PGVGV	PGGGV	902
QY	774	SGAG	779									
Db	903	GGGV	PG	908								

```

RESULT 11
US-11-053-100-32
; Sequence 32, Application US/11053100
; Publication No. US2005025554A1
; GENERAL INFORMATION:
; APPLICANT: CHIKORI, Ashutosh
; TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
; FILE REFERENCE: 4176-101 CIP
; CURRENT APPLICATION NUMBER: US/11/053,100
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 09/812,382
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,659
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 32
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(657)
; OTHER INFORMATION: PET17b-ELP4-120-Throm-T20 peptide
US-11-053-100-32

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Query Match	45.9%	Score 1913.5;	DB 11;	Length 657;
Best Local Similarity	60.0%;	Pred. No. 8.3e-125;		
Matches	492;	Conservative	65;	Indels 263; Gaps 68;
Oy	11	GSGVGVPVGVPGVGVPKGVPGVG-PGVG-PGVG-PGVG-PGAAGAGS	GAGAGS	66
Dd	3	GPGVGVPGVPGVGVPVGVPGVGVPGVGGVPGVPGVGV-----		48

[illegible]

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Publication No. US20050255554v1
GENERAL INFORMATION:
APPLICANT: CHIKOTI, Ashutosh
TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
FILE REFERENCE: 4176-101 CIP
CURRENT APPLICATION NUMBER: US/11/053,100
CURRENT FILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: US 09/812,382
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US 60/190,659
PRIOR FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn version 3.3
SEQ ID NO 29
LENGTH: 654
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic Construct
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)_(654)
OTHER INFORMATION: PET15b-ELP4-120-EK-T20 peptide
US-11-053-100-29

```

Query Match	45.8%	Score 1910.5	DB 11	Length 654
Best Local	59.7%	Pred. No. 1.3e-124		
Matches 491	Conservative	0	Mismatches 66	Indels 265
				Gaps 67

[illegible][illegible]

RESULT 14
US-11-053-100-38

```

Publication of: 7/27/2005
Publication No. US20050255554A1
GENERAL INFORMATION:
APPLICANT: CHIKKOTI, Ashutosh
TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
FILE REFERENCE: 4176-101 CIP
CURRENT APPLICATION NUMBER: US/11/053,100
PRIORITY FILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: US 09/812,382
PRIORITY FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US 60/190,659
PRIORITY FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn version 3.3
SEQ ID NO 38
LENGTH: 656
TYPE: PPT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic Construct
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(656)
OTHER INFORMATION: PET17b-ELP4-120-TEV(Q/Y)-T20 peptide
US-11-053-100-38

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[illegible]

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